

FOR OFFICIAL USE ONLY

ACCESS DB #

PLEASE PRINT CLEARLY

10/18 03p

10/19 1

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10-14-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 09/486,757
Location (Bldg/Room#): 2028 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Glycoline P-450 redox
Inventors (please provide full names): KUTCHAN et al.

Earliest Priority Date: 7-3-00

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 10

No size limits NA 2649
may

Please Include interference
Search.

Thanks

10/20/05
JH

RECEIVED

OCT 14 2005

TECH/CHEM. DIVISION
(STIC)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (C) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2005, 07:23:55 ; Search time 11004 Seconds
(without alignments)
11664.655 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2645.8	99.9	2650	8 PSU67185	U67185 Papaver som
2	1126.4	42.5	2498	8 AF302496	AF302496 Hybrid po
3	1104.8	41.7	2617	8 VIRNADHP4	L07843 Vigna radia
4	1094.8	41.3	2641	8 VSNER	Z26252 V.sativa nr
5	1086.2	41.0	2633	8 AY170374	AY170374 Glycine m
6	1071.6	40.5	2693	8 AB086169	AB086169 Ophiorthi
7	1061.4	40.1	2685	8 BT013756	BT013756 Lycopersi
8	1039	39.2	2079	8 AY596976	AY596976 Centauriu
9	1030.8	38.9	2059	8 AY520902	AY520902 Hypericum
10	997.2	37.6	2340	8 AY054688	AY054688 Arabidops
11	994.6	37.5	2079	8 BT008426	BT008426 Arabidops
12	987.6	37.3	2199	8 ATATRL1G	X66016 A.thaliana
13	985	37.2	2114	6 A75959	A75959 Sequence 1
14	969.8	36.6	2561	8 ECUE67186	U67186 Eschscholtz
15	918.6	34.7	2493	8 AF302497	AF302497 Hybrid po
16	912.6	34.5	2631	8 FM14CPR	Z49767 Pseudotsuga
17	911.2	34.4	2610	8 AF302498	AF302498 Hybrid po
18	895.4	33.8	2136	6 AX506108	AX506108 Sequence
19	895.4	33.8	2136	6 AX651759	AX651759 Sequence

20	895.4	33.8	2136	8 AF325101	AF325101 Arabidops
21	875.2	33.0	2556	8 AF024635	AF024635 Petroseli
22	875	33.0	2230	8 ATATR2M	X66017 A.thaliana
23	875	33.0	2423	6 A75961	A75961 Sequence 3
24	874	33.0	2466	8 AF024634	AF024634 Petroseli
25	873.6	33.0	2618	8 CRCPRA	X69791 C.roseus cp
26	867.4	32.7	2333	8 AF123610	AF123610 Triticum
27	864.8	32.6	2472	8 AY532374	AY532374 Ammi maju
28	862.4	32.6	2545	8 AF002698	AF002698 Pisum sat
29	859.8	32.5	2112	6 A75963	A75963 Sequence 5
30	852.6	32.2	2482	8 AK102060	AK102060 Oryza sat
31	850	32.1	2420	8 TAE303373	AJ303373 Triticum
32	808.4	30.5	2298	8 AK068915	AK068915 Oryza sat
33	808.4	30.5	2298	8 AK099083	AK099083 Oryza sat
34	807.6	30.5	1863	6 AR205034	AR205034 Sequence
35	807.6	30.5	1863	6 AR282641	AR282641 Sequence
36	807.6	30.5	1863	6 AX082548	AX082548 Sequence
37	807.6	30.5	1863	6 AX370663	AX370663 Sequence
38	807.6	30.5	1863	8 HTU2NFR	Z26250 H.tuberosus
39	659.2	24.9	1539	8 HTL2NFR	Z26251 H.tuberosus
40	606.6	22.9	1714	8 AK101320	AK101320 Oryza sat
41	586.4	22.1	2016	6 AX654074	AX654074 Sequence
42	569.6	21.5	2312	8 AF367288	AF367288 Arabidops
43	473.6	17.9	1023	8 AY059162	AY059162 Arabidops
44	295.8	11.2	715	8 HTU58629	U58629 Helianthus
45	282.4	10.7	1078	8 PAB132538	AJ132538 Picea abi

ALIGNMENTS

RESULT 1	PSU67185	Papaver somniferum NADPH:ferrihemoprotein oxidoreductase mRNA, complete cds.	2650 bp	mRNA	linear	PLN 06-MAR-1998
LOCUS	U67185					
ACCESSION	U67185.1	GI:2580496				
VERSION						
KEYWORDS						
SOURCE	Papaver somniferum (opium poppy)					
ORGANISM	Papaver somniferum					
REFERENCE						
AUTHORS	Rosco,A., Pauli,H.H., Priesner,W. and Kutchan,T.M.					
TITLE	Cloning and heterologous expression of NADPH-cytochrome P450 reductases from the Papaveraceae					
JOURNAL	Arch. Biochem. Biophys. 348 (2), 369-377 (1997)					
MEDLINE	98096363					
PUBMED	9434750					
REFERENCE						
AUTHORS	Rosco,A. and Kutchan,T.M.					
TITLE	Direct Submission					
JOURNAL	Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie, Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany					
FEATURES						
source	Location/Qualifiers					
	1..2650					
	/organism="Papaver somniferum"					
	/mol_type="mRNA"					
	/db_xref="taxon:3469"					
	/note="cell suspension culture"					
	124..2175					
	/EC_number="1.6.2.4"					
	/function="catalyzes the reduction of the heme-thiolate-dependent monooxygenases and oxidases; reduces cytochrome c"					
	/note="cytochrome P-450 reductase"					
	/codon_start=1					
	/product="NADPH:ferrihemoprotein oxidoreductase"					
	/protein_id="AAC05021.1"					
	/db_xref="GI:2580497"					
	/translation="MGSNNLANSIESMLGISIGSEVISDPIFIMVTTVASMLIGFGFF"					
CDS						

Qy	1921	ATTGCCCTTTTCACGTGAAGGGGAAAAGAGGAATATGTTTCAACATATAGATGATGGAGAAA	1981
Db	1921	ATTGCCCTTTTCACGTGAAGGGGAAAAGAGGAATATGTTTCAACATATAGATGATGGAGAAA	1980
Qy	1981	GCAACCGATGTATCGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGGTGATGCC	2040
Db	1981	GCAACCGATGTATCGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGGTGATGCC	2040
Qy	2041	AAGGGAAATGGCCAGAGATGTCATCGCACGTTGTCATACCATTTGCCCAAGAACACAGGGACCC	2100
Db	2041	AAGGGAAATGGCCAGAGATGTCATCGCACGTTGTCATACCATTTGCCCAAGAACACAGGGACCC	2100
Qy	2101	ATGGAATCATCTGCTGCCGAGCTGCAGTAAAGAACTCCAAAGTTGAAGAACGATATCTA	2160
Db	2101	ATGGAATCATCTGCTGCCGAGCTGCAGTAAAGAACTCCAAAGTTGAAGAACGATATCTA	2160
Qy	2161	AGAGATCTCTGGTGATCGAATGTAGCTTGCACAGTCCCTTTCTTGGCTGGTCTGTGTTA	2220
Db	2161	AGAGATCTCTGGTGATCGAATGTAGCTTGCACAGTCCCTTTCTTGGCTGGTCTGTGTTA	2220
Qy	2221	TGGTTTCTATTATATTAATTGATCTCTCTGAAATCCCAAGCACTTCCAGACATCCCTC	2280
Db	2221	TGGTTTCTATTATTAATTGATCTCTCTGAAATCCCAAGCACTTCCAGACATCCCTC	2280
Qy	2281	GATTCTTCTCCAGTGGTTCCAAATCGAAGCTCGTATAAATGAGAGCAGTGCAAATTGTG	2340
Db	2281	GATTCTTCTTCCAGTGGTTCCAAATCGAAGCTCGTATAAATGAGAGCAGTGCAAATTGTG	2340
Qy	2341	ACTACATGAGAGCAACACATCGAATACCATAGAAATAGAAAGATCAAAATTCCTTATCA	2400
Db	2341	ACTACATGAGAGCAACACATCGAATACCATAGAAATAGAAAGATCAAAATTCCTTATCA	2400
Qy	2401	GAACAAATGTTTACAGGCCAAAACTGTTTGCTTAATATAAAATTTTCACACCATGGGTGTGA	2460
Db	2401	GAACAAATGTTTACAGGCCAAAACTGTTTGCTTAATATAAAATTTTCACACCATGGGTGTGA	2460
Qy	2461	CAACACTGAAAAACAGTATTAGCTATACCAACAAAGTTATGCAAGGAAACACAAACTAGTTA	2520
Db	2461	CAACACTGAAAAACAGTATTAGCTATACCAACAAAGTTATGCAAGGAAACACAAACTAGTTA	2520
Qy	2521	GATCTTCTCTTTGGATGATTACTGTAAAGTTCTAAACAGATGATAGATTGTACTTAAAGA	2580
Db	2521	GATCTTCTCTCTTTGGATGATTACTGTAAAGTTCTAAACAGATGATAGATTGTACTTAAAGA	2580
Qy	2581	TTCTTGTTTCTTTATGGCTACCGAGAGGAGCTATATAATGCAATTTAGAGTTTTTGAGAAA	2640
Db	2581	TTCTTGTTTCTTTATGGCTACCGAGAGGAGTATATAATGCAATTTAGAGTTTTTGAGAAA	2640
Qy	2641	AAAAAAAAAAAA 2649	
Db	2641	AAAAAAAAAAAA 2649	

RESULT 2	AF302496	2498 bp	linear	PLN 13-DEC-2002
LOCUS	AF302496			
DEFINITION	Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome P450 oxydoreductase isoform 1 mRNA, complete cds.			
ACCESSION	AF302496			
VERSION	AF302496.1	GI:13183561		
KEYWORDS	.			
SOURCE	Populus balsamifera subsp. trichocarpa x Populus deltoides			
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.			
REFERENCE	1. (bases 1 to 2498)			
AUTHORS	Ro, D.K., Ehrling, J. and Douglas, C.J.			
TITLE	Cloning, Functional Expression, and Subcellular Localization of Multiple NADPH-Cytochrome P450 Reductases from Hybrid Poplar			
JOURNAL	Plant Physiol. 130 (4), 1837-1851 (2002)			
PUBMED	12481067			
REFERENCE	2 (bases 1 to 2498)			

Ro,D.-K. and Douglas,C.
 Direct Submission
 Submitted (05-SEP-2000) Botany, University of British Columbia,
 6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
 Location/Qualifiers
 1..2498
 /organism="Populus balsamifera subsp. trichocarpa x
 Populus deltoides"
 /mol_type="mRNA"
 /db_xref="taxon:3695"
 84..2162
 /note="CPRI; enzyme"
 /codon_start=1
 /product="NADPH-cytochrome P450 oxidoreductase isoform 1"
 /protein_id="AAK15259.1"
 /db_xref="GI:13183562"
 /translation="MSSGGSNLARFVQSVLGISFGDSLSDSVVVIITSPFALVGLVW
 LVLRSSDRSDKVPKLVWPKSLIKDEESENALGCKTKVIFYGTQTGTAEGFAKAL
 ABEVKARYEKAIVKVPDLDDYAWEDDQYEKKETLALFWAYDGGEPDPAARYF
 KMTFEGNERGILWQLSYGVFGLGNNRQYEHFNKIAKVLDDLWYVQGGEPDPAARYF
 DCLANGDSFAWEKFLWPELQDLRLDRDDVNA PSTTAAIPEYRLVHIQPSIISVEDK
 FSNLANGVSYFOIHHPCRVNNAVKQELHKAESRSCIHLEFDITGTGITYETGDHGLV
 YAENSDTEVEAKDLKDPDLILFTHADNEDGTAIGSSLPPFPQGPCTLHTALACVA
 DILSPPKKALALAAHASEPSEADPLKLSPPQCKNEYSHWMAQSRLSLEYMAEFP
 SKPPLGIFTFAAEPRLQRYYSISSPRTFNHVHTALVTGPTITGRHKGVCST
 WKNAVPLKSEYECVMAPIFTKTSNPLKPADPSTPLIMVPGTGLAPFFGFLQERLAL
 KEDGPKGLPALLFGCGRNRMDFIYEDELNNFVEQVISELIVAFSREGPQKEYVQHK
 MYDRAAEIWTIITSQGGYFVCGDAKGMDRVHRTLHTIIVQEQGGLDSKSTESMVKVGLQ
 MEGRYLVDPVM"
 CDS
 source

ORIGIN

	Query Match	42.5%;	Score 1126.4;	DB 8;	Length 2498;
	Best Local Similarity	72.2%;	Pred. No. 2.7e-254;		
	Matches 1517;	Conservative 0;	Mismatches 556;	Indels 27;	Gaps 3;
QY	105	TTCCAGAGTCTCTGCTAAATATATGGTTTCGAATAATTTAGCTAATTCGATTGAATCGATGTT	164		
DB	71	TTCTTAATCAAGATGAGTTCAGGTGTTCAAAATTTGGCGAGGTTCGTTCAATCAGTGCT	130		
QY	165	AGGATATCAATFAGGATCAGATATATATTTCTGACCCAAATTTTTCATTTATGGTCAACAATGTT	224		
DB	131	AGGGATATCTTTTGG--CGACTCCCTGTCTGACTCAGTTGTGTGATAATTACCACTG	187		
QY	225	AGCTTCAATGCTGATTGGAAATTTGTTTCTTCGCATGATGAATCTTCGTTCTTCTCAATC	284		
DB	188	GTTTGTGCTCTAGTTTGGATTTGGTGTGCTGTGATTGAAGAGATCGTCCGATCGGAGCAA	247		
QY	285	AAAACTTA-----TTGAAACTTATAAACCAATAATTTGATAAAGAAAGAGAGAGAT	335		
DB	248	AGACGCTCAAGCGCTTGGTGGTTCCTAAAGTCACTTTTCAATTTAAGGACGAGGAGATCGATC	307		
QY	336	TGAAGTTGATCTCGTAAATTAAGCTCACTATATTTTTTGGTACTCAGACTGGTACTGC	395		
DB	308	CGAGGCTCTGGGTGGGAAACCTAAGGTACTACTCTTTTATGGGACTCAGACCGGAAGTGC	367		
QY	396	TGAAGGATTTGCTAAAGGCAATTGGCAGAGAAGAAATTAAGGCCAAAGTACAAGAAAGCAGTTGT	455		
DB	368	GGAGGTTTTTGTCTAAGGCTTTTAGCTGAAGAGGTCAAAGATATGAGAAAGCAGCTGT	427		
QY	456	TAAAGTAGTTGACCTTGGATGACTATGCAGCCGAGGATGATCAATATGAAGAGAAATTAAT	515		
DB	428	TAAAGTTTGTACCTGGATGATATGCTATGAAGAGATGATCAATATGAAGAAATTTGAA	487		
QY	516	GAAGAGTCTTTTGGTGTTTTTTCATGGTAGCCACTTATGGTGTAGTGGTACGCCAACTGACAA	575		
DB	488	GAAGAGACTTTTGGCATTTATCATGGTTGCCACTTATGGAGATGGAGAGCCAACTGATAA	547		
QY	576	TGCTCGGAGATTTTCAAAATGGTTCACTCAGAGAAATGAAGGGGAGAGTGGCTTCAGCA	635		
DB	548	CGCTCGGAGATTTTATAAGTGGTTTACTGAGGGAAATGAAGGGGGAATCTGGCTTCAACA	607		
QY	636	ACTTAACATTTATGGTGTTTTTTGGTGTAAACCGTCAATACGAGCATTTTCAAACAAGATCG	695		

Db 608 GCTTTCTTATGGTGTCTTTGGTCTTGGTAAACCGTCAATATGAACATTTTAAATGAATAGC 667

Qy 696 GGTAGATGTGGATGAGCAACTCGGTAAACAAGGTGCAAAAGCGCATGTTTCAAGTGGGGCT 755

Db 668 GAAGGTGCTTGTATGACCTGCTCTATGAACAAGGAGGAACGCTCGTTCTCTGTGGTCT 727

Qy 756 CGGTGAGGATGATCAATGCAATGAAGATGATTTTACTGCTTGGCGAGAAATGTTGTGGAC 815

Db 728 TGGCGAGGATGATCAATGCAATGAGGATGATTTTCTGCTTGGAAAGAAATTTTGTGGCC 787

Qy 816 TGAATGGATCAGTTGCTCAAAAGATGAGGATGCTGCTCCTTCAAGTGGCTACACCGTATAT 875

Db 788 TGAGCTAGACAGTGTGCTCAGAGATGAAGATGAATGCTCCATCTACTCCTTATAC 847

Qy 876 TGCTACTGTTCTGGAATACAGGGTGTGATTTCCAGAAACTACCGGTCCGCGCTCTGGATGA 935

Db 848 AGCTGCTATACCTGAAATATCGAATAGTGTAGTGAATCATGATCCTTCTATAATATCTCTTGAGGA 907

Qy 936 TAAACATAAATACTGCTAAACCGGATGTTGCAATTTGATATTTCTCCATCCTTGCAGAAC 995

Db 908 TAAATTTCTCAAACTTGGCAATGGGAATGTGTCTTTTGATATTTCAACCATCCATGCGAGT 967

Qy 996 CATTTGTTGCTCAACAAGAGAGCTCCACAAACCCAAAGTCTGTAGATCCTGTATACATCT 1055

Db 968 CAATGTTGCTGCCAAAAGAGCTTCAAAAGCAGAGTCTGACGGTCTTGCAATACATCT 1027

Qy 1056 GGAAGTTCGACATACAGGCTTCTCCCTTACATATGAGACTGGAGATCATGTTGGTGTFTA 1115

Db 1028 GGAATTTGACATCACAGGACTCGAATTAATATGAAATCGGAGACCAATTTGGGGGTGA 1087

Qy 1116 TGCTGAGAACTCGGATGAACACTCTCGAGGAGCAGGAGAGCTGTTGGTCAACCCCTGA 1175

Db 1088 TGCTGAGAACTAGTGAAACTGTGAAAGAGCAGGAGTGTCTAGATAAACCTTTAGA 1147

Qy 1176 TTTGCTGTTTTCAATCACACGGATAAAGAGCGGTACCCACGAGAGCTCAATTACC 1235

Db 1148 TTTGTTGTTTCTATTCATGCTGATATGAGATGSCACAGCTATTGGAGCTCATTGCC 1207

Qy 1236 ACTCTCTTCCAGGCTTGTGACCTTACGATCTGCGCTAGCAGCTATGCTGATCTTTT 1295

Db 1208 GCCTCTCTTCCAGGTCCTCGCACACTTCACACTGCAATGGCATGCTATGACAGATCTTT 1267

Qy 1296 GAATCTCTTAGAAGGCTCTCTGATGCTCTGTCGGCTCATGCTATGTCACCCAGTGA 1355

Db 1268 GAGCCCTCTTAAAGAGCTCTTGTGCTGTTGGTGTCTATGCGCAGTGAACCTTAGCA 1327

Qy 1356 AGCAGAGAGATGGCTTTTTTGTTCATCACCTCTGGGAAAGATGAGTATTCAAAATGGGT 1415

Db 1328 GGCAGATAGACTCAAGTTTTTATCATCACCGCAAGGAGAAAGATGAATACTCTCACGCGT 1387

Qy 1416 AGTTGGAAGTCAGAGGAGTCTTTTGAGATCATGCGCGAGTTCATCAGCAAAACCCCC 1475

Db 1388 CATGGCAAGTCAGAGAAGTCTTCTCGAGGTAATGGCTGAGTTCCTCATCTTCGAAACCTCC 1447

Qy 1476 TCTTGTGTGCTCTTGTCTGCACTGACCCCTCGCTTACCGCTCGATCTATTTCTATCTC 1535

Db 1448 CCTTGGTATCTTTTGTCTGAGTGGCTCTCTCGCTACAGCCCTCGTACTATTTCTATCTC 1507

Qy 1536 ATCCTCTCTCAAGTGTGCTCCCTCAAGAAATTCATGTGACGTGTGCTTTTAGTATATGGTCA 1595

Db 1508 ATCCTCTCTAGATATACTCCCAATAGAGTACATGTGACCTGTGCTTTAGTATATGGTCC 1567

Qy 1596 AAGCCCTACCGAAGGGTTTACCGAGAGAGTGTGTTGACATGATGAAGATCAGTGTCC 1655

Db 1568 AACTCCCACTGGTAGAATTCACAAAGGGGTGTGTTCAACTTGGATTGAAGAAATCAGTTC 1627

Qy 1656 TCAGGA-----TAGCTGGGCTCTCTATTTTGTTCGAACGTCGAACCTTCAA 1700

Db 1628 TCTGGAGAAAGTATGAATGTAGTTGGGGCTCCCAATTTTCCACAGAAACATCTAATTTCAA 1687

Qy 1701 GTTACAGGCTGACCCCTCAACTCCAATTTATCATGGTGGGACCTGGTACAGGGTTAGCTCC 1760

Db 1688 GTTACCAGCAGATCCTTCAACTCCAATTAATATGTTGGGTCTCTGGTACTGGATTGGCACC 1747

RESULT 3
VIRNADPH4
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

VIRNADPH4 2617 bp mRNA linear PLN 23-APR-2001
Vigna radiata NADPH cytochrome P450 mRNA, complete cds.

L07843
L07843.1 GI:295447

Vigna radiata

Vigna radiata

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.

1 (bases 1 to 2617)

Shet,M.S., Sachseivan,K., Arlotto,M.A., Mehdy,M.C. and
Estabrook,R.W.

Purification, characterization, and cDNA cloning of an
NADPH-cytochrome P450 reductase from mung bean

Proc. Natl. Acad. Sci. U.S.A. 90 (7), 2890-2894 (1993)

93219390

8464904

Location/Qualifiers

1..2617

/organism="Vigna radiata"

/mol_type="mRNA"

/cultivar="berken"

/db_xref="taxon:157791"

/dev_stage="7 day etiolated seedling 15 hr after wounding"

1..174

/codon_start=1

/product="NADPH cytochrome P450"

/protein_id="AAA34240.1"

/db_xref="GI:295448"

/translation="MASNSDLVRAVESFLVSLGDSVSDSLLLIATTSAAVVVLLVLF
LWKSSDRSKVPPVPRDLMMEEVEVDVAAKTKVTTFGTOTGTAEAGFALALAE
ETKAYEKAAVVDLDYADDDLVEEKLKESELVFFMLATYGDEPTDINAARFYKW
FTGKDEGCIWKLTYTGYGLNQRQYEHFNKIKGVDBELAEQAGKRLVAVGLGDD
QSIDDFSAWSELSWELQDLURDDANTVSTPTAAILEYRVVHDFTAASTYDNH
STVANGTEFDIHFPKRVNVAQKELHKPESDRSCIHLEFDISGTSITDTGHHGVY
AENCNTEETKLLGQNLDFLSLTKDDGTSGLGSLPFPGPFCSLRTALARYAD
LINPRKAAIALALATHASPSDERLKLSSSQKDEYSKWVVGVSQSLVENVAAFPFA
KPPLGVFFAAIAPRIQPRYSISSSPRFPAPQRVHVTCALVYGTPTPTGRHKVCSTWM

5' UTR
CDS

source

FEATURES

PUBMED

MEDLINE

JOURNAL

TITLE

AUTHORS

REFERENCE

3'UTR
polyA site

Qy	908	ACGAAACTACGGTCGCGGCTCTGATGATAAACACATATAATATCTGCTAACCGCGATGTTG	967
Db	1001	ATGATTCCACCGTCACATCTTTGCAATGATTAATCACTTAATATGTGGCAATGGTAATGCTG	1060
Qy	968	CATTGTGATATCTCCATCTTTGCAGAACCATTTGTGTCTCAACAAAGAGAGCTCCACAAAC	1027
Db	1061	TGTTTGATATTCACCATCTCTTGACGGGTAAATATGCCGCTCAAGAGAACTTTCCAAAC	1120
Qy	1028	CCAAGTCTGATAGATCCCTGTATACATCTGGAGTTGCACATATCACGGCTCTTCCCTTACAT	1087
Db	1121	CTGAGTCTGATCGTTCTTTGATACATTTTGAGTTTGACATATCGGGACTGGGATTAATAT	1180
Qy	1088	ATGAGACTGGAGATCATGTTTGGTGTATAGCTGAGAACTCGATGAAACTGTCTGAGGAAG	1147
Db	1181	ATGAAACTGGTGACCATGTGGGTGTTTTTGTCTGAAACCGCGATGAACTGTTTGAAGAAG	1240
Qy	1148	CAGGAGCTGTGGGTCAACCCCTGGAATTTGCTGTTTTCAATTTACACGGATAAAGAAG	1207
Db	1241	CTGGAAGTTGCTGGGTGAGATTAGATTGGTATTTTCCATTTCACTCACTAAATATGAGG	1300
Qy	1208	ACGGGTCACCCCAGGAAGCTCAATTACCACTCTCTTTCCCAAGTCTCTTGCACTTACGAT	1267
Db	1301	ATGGTACTCTCTAGGAAGTTCTCTGCCACTCTCTTTCTGTGCCCTTGACACTGGCT	1360
Qy	1268	CTGCCCTAGCA CGCTATGCTGATCTTTTGTGAATCTCTCTAGAAAGGTTTCTCTGATTGCTC	1327
Db	1361	TTGCTTTGGCACATTAATGCAGATCTCTTGAATCCCCACGCAAGGCTTCTTTAGTGGCTC	1420
Qy	1328	TGTCGCTCATGATCTGTATCCAGTCAAGACAGAGATTTGCGCTTTTGTCTCATCACTTC	1387
Db	1421	TGGCTGCACATACTCTGGAAACCCAGTGAAGACATAGATTAAACATTCCTCTCATCTCCTC	1480
Qy	1388	TGGAAAGAAATAGATAATCAAAATGGGTAGTTTGGAACTCAGAGAGTCTTTTCGAGATCA	1447
Db	1481	AGGGAAGGATAGTACTCCAAATGGCTGTGGGAAGTCAAGAGAGTCTCTTTGAGGTAA	1540
Qy	1448	TGGCCGAGTTTCANACAGAAACCCCTCTTGGTGTGTTCTTTGTCTGCAAGTAGCCCTC	1507
Db	1541	TGGCTGAGTTTCGTCTAGCAAAACCCGCTTGGTGTGTTTTTTTGTCTGCAAGTAGCCCTC	1600
Qy	1508	GCATTACCGCTCGATACTATTCTATCTCATCTCTCTCTAAAGTTTGTCTCCCTCAAGAATTC	1567
Db	1601	ACTTACAACCTCGTTATTATTCTATTTCATCTCGCTAGGTTTTCCCCCAAAAGGTGC	1660
Qy	1568	ATGTGACGTGTGCTTTTAGTATATGGTCAAAAGCCCTACCGGAAGGTTTCACCGAGGAGTGT	1627
Db	1661	ATGTAACTTTGTGCCTTGGTATGTGTTCCAACTCTCTACTGGAAGAAATTCACAAAGGAGTAT	1720
Qy	1628	GTTTCGACATGGATGAAGCATGCAAGTTCC-----TCAGGATAGCTGGGCTC	1672
Db	1721	GTTCAACCTCGATGAAGAAATGGCAATTCCTTAGAGAAACCGGTGACTGTAGTTGGGCTC	1780
Qy	1673	CTATTTTTTGTTCGAACGTCAAACTTCAAGTTTACCAGCTGACCCCTCAACTCCAAATATATCA	1732
Db	1781	CTATTTTATACAGAAATCAAACTTCAAGTTTACAGCTGATCATTCATTCCTATTATTA	1840
Qy	1733	TGTTGGGACCTGGGTACAGGGTTAGTCTCTTTTCAGAGGATTTCTGCAAGGAAGAAATGGCCC	1792
Db	1841	TGTTTGTCTCTGGTACAGGCTGSCACTTTTCAGGGGATTTTTACAGGAAGAAATTTGGCCC	1900
Qy	1793	TCAAGGAAATGGTGTCTCAACTTTGGCCCCAGAGTGTCTTTTTTCGGATGTAGGAATCGTA	1852
Db	1901	TCAAGAGGATGCGGTTCAACTTTGGTCTCGATTTACTCTTTTGGATGTAGGAATCGAC	1960
Qy	1853	ATATGGACTTCAATTATGAAGACGAACCTAAACAACCTTGTGGGAACGAGGAGTCAATTCGG	1912
Db	1961	AAATGGATTTTATTTATGAGGATGAGCTAAGAAATTTTATGGAAACAGGTGCTCTGTACG	2020
Qy	1913	AGCTAGTTATTTGCCCTTTTCA CGTGAAGGGGAAAGAAAGGAATATGTTTCAACAATAAGATGA	1972
Db	2021	AGTTGATAGTCACAATTCTCGAGAGAGGGA CTTGAAAGGAGTATGTTTCAACAACAAGATGA	2080

Qy	1973	TGAGAAACCAACGAGTATGAATGTGATATACAGGAGCGGTATCTCTATGTGTGTG	2033
Db	2081	TGATAAAGCTGCAAAATCTGTGGAATTTGATTTCTCAGGAGAGTTATCTTTATTTGTG	2140
Qy	2033	GTGATGCCAAGGAAATGGCCAGAGATGTCCATCGCAGTTTGCATACCAATGCCCAAGAAC	2092
Db	2141	GTGATGCTAAGGCAATGGCCAGAGATGTTTCATCGGACTCTTCATACCAATGTCCAGCAGC	2200
Qy	2093	AGGAGCCCATGGAAATCATCTGTCTGCCGAAGCTGCAGTAAGAAACTCCAAAGTTGAAAGAAC	2152
Db	2201	AGCAAAATGTGGACTCTTCAAGGCGAGAGCTATAGTTTAAAAAACTCCAGATGGATGGAC	2260
Qy	2153	GATATCTTAGAGATGTCGTGGTGA	2175
Db	2261	GTTATCTTAGAGATGTCGTGTAA	2283
RESULT 6			
AB086169			
LOCUS	AB086169	2693 bp	mRNA linear PLN 13-MAY-2003
DEFINITION	Ophiorrhiza pumila cpr mRNA for NADPH-cytochrome P-450 reductase, complete cds.		
ACCESSION	AB086169		
VERSION	AB086169.1	GI:26106070	
KEYWORDS			
SOURCE	Ophiorrhiza pumila		
ORGANISM	Ophiorrhiza pumila		
REFERENCE	1		
AUTHORS	Yamazaki, Y., Sudo, H., Yamazaki, M., Aimi, N. and Saito, K.		
TITLE	Camptothecin Biosynthetic Genes in Hairy Roots of Ophiorrhiza pumila: Cloning, Characterization and Differential Expression in Tissues and by Stress Compounds		
JOURNAL	Plant Cell Physiol. 44 (4), 395-403 (2003)		
MEDLINE	22608538		
PUBMED	12721380		
REFERENCE	2		
AUTHORS	Yamazaki, Y., Yamazaki, M. and Saito, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-JUN-2002) Mami Yamazaki, Graduate School of Pharmaceutical Sciences, Chiba University, Department of Molecular Biology and Biotechnology; 1-33 Yayoi-cho, Inage-ku, Chiba-shi, Chiba 263-8544, Japan (E-mail:mamiy@p.chiba-u.ac.jp, Tel:81-43-290-2905, Fax:81-43-290-2905)		
FEATURES	Location/Qualifiers		
source	1..2693		
	/organism="Ophiorrhiza pumila"		
	/mol_type="mRNA"		
	/db_xref="taxon:157934"		
gene	1..2693		
	/gene="cpr"		
CDS	142..2214		
	/gene="cpr"		
	/codon_start=1		
	/product="NADPH-cytochrome P-450 reductase"		
	/protein_id="BAC41516.1"		
	/db_xref="GI:26106071"		
	/translation="MDTKLELPIESALGVSIGDDVNOILVLITSLAVIVGLMLPFLWKSGDRGKEIKFVPGSGCCALLVEEKEVDFTKVVTFPGTGTAGTAFKALSEEFTKARYEKAVKVFVDLDDVYAADNDQYEEKLKGTLAFMLATYGDGETDPAARFKYKFTIGKEREPLVQQLTYGVGADNQRQYEHFNKINVIHQELSEGAKRIVPGLGDDQFCTIEDDFAWREQLWPELDQTLRDDDATSAATPYTAAILERYVIVHNSEAASVDKQFVSMANGNSVDYIHPCTVGNVAQRELHKPSDRSCIHLEFISGTINVTGADHVGVYADLENCDGTVEQAQVLPDLVDFIHADKEDTSLGSLGDPFPFGPSLRTALARYADLKNYPKAAALVALAAHSESEASBELKFLSPQCKDEYAOGIVGNKSLLEWAEFSAKLPFGVFFAAMFRLPPRYISISSFPAPNVRHVTCALVYGPTPGRIHKGICSTWMAVPSERSHESKCAPIFKSSNFKLPADEPTPIIWWGPTGLAPFRGFLQERLAKKEIKVAGLQALGHALFFCCRNRMDFIYELSGRNQGVISLIVAFSRGPGQKEYVQHKQMTDKKAAQFWSLISQVGYLVYCCDAKGMDARVHRTLTHTIYVQENVDSSKAAEIVVKLODTGRYLVDVW"		

ORIGIN

Query Match 40.58; Score 1071.6; DB 8; Length 2693;
Best Local Similarity 73.94; Pred. No. 2.1e-241;
Matches 1381; Conservative 0; Mismatches 474; Indels 15; Gaps 1;
Qy 322 GAAGAAGAGAGATTGAAGTTGATCTCTGGTAAATTAAGCTCACTATATTTTGGTACT 381
Db |||||
Qy 346 GAGGAGAAAGGAGAGTGGATCTTAAAGTTAAAGTTACGGTCTTTTCGGTACT 405
Db |||||
Qy 382 CAGACTGGTACTGCTGAAGGATTGCTAAGGCAATGGCAGAGAAATTAAGCAAGTAC 441
Db |||||
Qy 406 CAGACTGGTACTGCTGAGGAGGTTTGTAAAGGCAATGGCAGGAGATCAAGGCGAGATAT 465
Db |||||
Qy 442 AAGAAAGCACTGTGTAAGTAGTTGACCTGATGACTATACGCCGAGGATGATCAATAT 501
Db |||||
Qy 466 GAGAGGCACTGTTTAAAGTTTGAATTTGGATGATATGCTGCAGATGATGATCAGTAC 525
Db |||||
Qy 502 GAAGAGAAATTAAGAAAGAGTCTTTGGTGTGTTTTCATGTTAGCCACTTATGGTGTGTT 561
Db |||||
Qy 526 GAGGAAAGCTGAAGAAAGAAACACTGGCAATCTTCATGTTGGCACTTATGAGATGA 585
Db |||||
Qy 562 GAGCAACTGACAACTGCTGAGATTTTACAATGGTTTCACTCAGGAACATGAAGGGGA 621
Db |||||
Qy 586 GAGCGACTGACAACTGCGCCAGATTTTACAATGGTTTACAGAGGAAAGAGAGGAA 645
Db |||||
Qy 622 GAGTGGCTTACGCACTTACTATGTTGTTTGGTGGTAAACCGTCAATACGAGCAT 681
Db |||||
Qy 646 CCTGGCTTACGCACTTACTATGTTGTTTGGTCTGGGAAACCGCAATATGAGCAT 705
Db |||||
Qy 682 TTCAACAAGATCGCGTAGATGTGGATGAGCAACTCGGTAAACAAGGTGCAAAAGCGCAT 741
Db |||||
Qy 706 TTCAATGAATTTGGAAAGCTGATTCATGAGCAACTAAGTGACAGGTGCAAAAGCAT 765
Db |||||
Qy 742 GTTCAAGTGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTGGCGA 801
Db |||||
Qy 766 GTTCCAGTTGGCTCTGGAGATGATGATCAGTGTATCAGGATGATTTTGTGCTGGCGA 825
Db |||||
Qy 802 GAATGTTGGGACTGAATTTGGATGAGTCTCTCAAGATGAGTGTCTCTTCACTG 861
Db |||||
Qy 826 GAACAATGTGGCTGAATTTAGATCAGATACTCAGAGACGAGATGATGCAACTCGGCG 885
Db |||||
Qy 862 GCTACACCGTATATTTGCTACTGTTTCTGTAATACAGGAGTGTGATTCACGAAATACGGTC 921
Db |||||
Qy 886 GCTACCCCTTACTGCTGCAATCTTGATATATAGATGATTAATTTCTAGGCT 945
Db |||||
Qy 922 GCGGCTCTGATGATTAACAACATAAATGCTGTAACGGCGATGTTGCAATTTGATTTCTC 981
Db |||||
Qy 946 GCATCTTACGAGATAAGCAATTCAGCATGGCTTAACGGGAACTCCTCATATGATATTTAT 1005
Db |||||
Qy 982 CATCTTGCAGAACCATTTGCTTCAACAAGAGAGCTCACAACCCAGTCTGATAGA 1041
Db |||||
Qy 1006 CATCCATGCAATGATTAATGTTGCTTCAAGAGAGCTTCAAGGCTGAACTCTGATCGC 1065
Db |||||
Qy 1042 TCCTGTATACATCTCGAGTTTCGACATATCAGGCTCTTCCCTTACATATGAGCTGGAGAT 1101
Db |||||
Qy 1066 TCATGATCACCCTGGNAATTTGATATATCTGGCACAGGCAATTAATTAAGAACTGGAGAC 1125
Db |||||
Qy 1102 CATGTTGGTGTATGCTGAGAACTGCGATGAACTGTGAGGAAGCAGGAGCTGTTG 1161
Db |||||
Qy 1126 CATGTTGGGCTTTATGCTGAAATTTGTATGGAATCTGTTGAGCAAGCAGCAAAAGTTG 1185
Db |||||
Qy 1162 GGTCAACCCCTGATTTGCTGTTTTCATTTCAACGAGTAAGAACGGGTCAACCCAG 1221
Db |||||
Qy 1186 GGTCAACCTTTGATTTTGTATTTTCTATCTCATGCTGATAAAGAGATGTTAGTCACTT 1245
Db |||||
Qy 1222 GGAAGCTCATTAACACTCTCTTCCAGGCTCTTGGACCTTACGATCTGCTTAGCAGCG 1281
Db |||||
Qy 1246 GGAAGCTCATTAACACTCTCTTTCAGGCTCTTTCAGGCTCTGCTACTGCTTGTCTGCG 1305
Db |||||
Qy 1282 TATGCTGATCTTTGATCTCTCCTAGAAAGGCTTCTCTGATTTGCTCTGCTCGCTATGCA 1341
Db |||||
Qy 1306 TATGCGATCTTCTGAATTAACCTCGAAAGGCTGCTTTGTTGCTATTAAGTCTGCTCATGCA 1365
Db |||||

Qy 1342 TCTGTACCCAGTGAAGCAGAGAGATTGGCGTTTGTGTCATCACTCTGCGAAAGATGAG 1401
Db |||||
Qy 1366 AGTGAACCTAGTAGAAGCAGAAAGGCTAAAGTTCTTGTTCATCACTCAGGAAAGATGAG 1425
Db |||||
Qy 1402 TATTTAAAATGGGTAGTTGGAAGTCAAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCA 1461
Db |||||
Qy 1426 TACGCACAGGAGTTGTTGAAACACAGAAAGTCTTCTTCAAGGTTATGGCTGAGTTTCT 1485
Db |||||
Qy 1462 TCAGCAAAACCCCTCTTGGTGTGTTCTTGGTGCAGTAGCCCTCTGCTTACGCCCTCGA 1521
Db |||||
Qy 1486 TCAGCAAAACCCCTCTTGGTGTGTTTTCAGCAATGGCCCTCTGCTTACCAACACGGA 1545
Db |||||
Qy 1522 TACTATTCTATCTCATCTCTCTTAAGTTTGGTCCCTCAGAAATTCATGTGAGCTGTGCT 1581
Db |||||
Qy 1546 TATTATTCTATCTCTCTTCCGCCAGATTTGCTCCAAATAGAGTTTCAATGTAAGCTGTGCC 1605
Db |||||
Qy 1582 TTAGTATATGGTCAAAAGCCCTACCGAAAGGTTTCAACGAGAGTGTGTTCCGACATGATG 1641
Db |||||
Qy 1606 TTGGTGTATGGGCCAATCTCAACTGGACGTTTTCACAAAGGCATATGTTCCGACATGATG 1665
Db |||||
Qy 1642 AAGCATGCAAGTTCC-----TCAGGATAGCTGGGCTCTCTATTTTGTTCGA 1686
Db |||||
Qy 1666 AAGAAGCCAGTTCCATCTGAGAAAGCCACAGTGCAGCAAGGGCTATTTTATCAGA 1725
Db |||||
Qy 1687 AGCTCAAACTTCAAGTTTACAGCTGACCCCTCACTCCAAATTCATGTTGGGACCTGCT 1746
Db |||||
Qy 1726 TCTTCAATTTTCAAAATTAACCTGCTGATCTCTTACCTCAATTCATGTTGGGACCTGGG 1785
Db |||||
Qy 1747 ACAGGGTTAGCTCTCTTTCAGAGATTTTCGACGAAAGATGCTCCCTCAAGGAAATGCT 1806
Db |||||
Qy 1786 ACGGCTTGGCTCATTAGAGGATTTTACAGAGAGATTTGGCTTGAAGAATTTGGGA 1845
Db |||||
Qy 1807 GCTCAACTTGGGCCCAAGAGTGTCTTTTTCGGATGATGAGGATCGTAAATATGAGCTTCATT 1866
Db |||||
Qy 1846 GCTCAGCTTGGTCCCGCTTTTATGTTCTTTGTTGTCAGAAACCGCAGAAATGGAATTTAT 1905
Db |||||
Qy 1867 TATGAAGACGAACTAAACAACCTTCGTGGAAACGAGGAGTCAATTCGGAGCTAGTTATTTGCC 1926
Db |||||
Qy 1906 TATGAGATGAGCTGAGTGTGTTTGTCAATCAAGGAGTAAATTCAGAGCTTATTTGTGCA 1965
Db |||||
Qy 1927 TTTTCACTGGAAGGGGAAAGAGGAAATATGTTTCAACATAAGATGATGGAAGAAAGCAACG 1986
Db |||||
Qy 1966 TTTTCTCGTGGGGGCCACAGAGGAGTATGTCACATAAGATGACAGAGAGGCTGCT 2025
Db |||||
Qy 1987 GATGTAAGAAATGTGATATACAGGGGACGGTATCTCTATGTTGTGTTGATGCAAGGGA 2046
Db |||||
Qy 2026 CAATCTGGAGTTTGATCTCCCAAGTGGGTATCTTTATGTTTGTGGGACGCAAGGGG 2085
Db |||||
Qy 2047 ATGGCCAGAGATGTCATCGCAGTTCATCCATTCGCAAGAAAGAGGACCCATCGAA 2106
Db |||||
Qy 2086 ATGGCAAGAGATGTGATCGCATCTTTCATATCTTTCAGAGCAGGAAATGTCGAT 2145
Db |||||
Qy 2107 TCATCTGCTGCCCAAGCTGCAAGTAAAGAACTCCAAAGTTGAAGAAAGATATCTAAGAGAT 2166
Db |||||
Qy 2146 TCTCGAAGCTGAGGCCATTGTGAAGAAACTACAGACGACGGGCGATATCTCAGGGAT 2205
Db |||||
Qy 2167 GTCTGTGAT 2176
Db |||||
Qy 2206 GTGTGTGAT 2215
Db |||||

RESULT 7

BT013756
LOCUS
DEFINITION
Lycopersicon esculentum clone 132622F, mRNA linear sequence.
ACCESSION
BT013756
VERSION
BT013756.1
KEYWORDS
FLI_CDNA, GI:47105171
SOURCE
Lycopersicon esculentum (tomato)
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.	
1. (bases 1 to 2685)	
Kirkness, E.F., Wang, W. and Vazeille, A.	
Direct Submission	
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712	
Medical Center Drive, Rockville, MD 20850, USA	
Location/Qualifiers	
source	
1..2685	
/organism="Lycopersicon esculentum"	
/mol_type="mRNA"	
/db_xref="taxon:4081"	
/clone="132622P"	
/tissue type="fruit"	
/note="TZBW29"	
ORIGIN	
Query Match	40.1%; Score 1061.4; DB 8; Length 2685;
Best Local Similarity	73.1%; Pred. No. 5.4e-239;
Matches 1397; Conservative	0; Mismatches 496; Indels 18; Gaps 2;
QY	281 AATCAAAACCTATTGAACTTATAAACCAATAATTGATAAAGAAAGAGGAGATTGAAG 340
DB	1177 TTGATATATCTGGCACTGGGATTTCTATGAAACAGGAGATCATGTGGGTGTTATGCTG 1236
QY	400 AAGTGAAGCCGTGGTGTTCCTCCCAAGTCTTACATGTGGAGCCGAGAGGAGACTGAGC 459
DB	1121 AGAAGTGGCGATGAAACTGTGCGAGGAAGCAGGAAAGCTGTGGGTCAACCCCTGGATTGC 1180
QY	341 TTGATCCTCGTAAATTAAGCTCACTATATTTTGTGTAAGTCTGAGCTGCTGCTGAAG 400
DB	1237 AAAATCTCTGAAGATACTGTGTAGGAAGCTGCGAGATTGTGGGGCAGTCATTAGACTTGA 1296
QY	460 TAGAACCCTGGAAAGTTAAGGTCAACCGTATTTTTCGGTACTCAAACTGGTACTGCTGAGG 519
DB	1181 TGTTCCTGATTCACACGGATAAAGAAAGAGCGGTCAACCCAGGGAAGCTCATTTACCACTC 1240
QY	401 GATTTGCTAAGGCATTTGGCAGAGAAATTAAGGCAAAAGTACAAAGAGAGAGTGTGTTAAAG 460
DB	1297 TATTCCTCTATTATACCGCAAGAGGAGATGGTACAGCTGAGAGGAGCTGTTACCCCCAC 1356
QY	520 GTTTTGCCAAAGCTTTATCAGAGGAGATAAAGCAAGATATGAGAGGCGATGTGTGAAG 579
DB	1241 CTTTCCAGGTCTCTTGACCTTTACGATCTGCGCTTAGCAGCGCTATGCTGATCTTTTGAATC 1300
QY	461 TAGTGACCTGGATGATCTATGACCGAGAGATGATCAATATGAAGAGAAATTAAGAAAG 520
DB	1357 CTTTTCCTGGTCCCTGCACTCTACGTGCTGCACTGCTTGTATTATGAGATCTTCGAATC 1416
QY	580 TCGTGACATGGATGATTATGCTGCCGATGATATTTACGAGGAGAGAACTGAAGAAAG 639
DB	1301 CTCCTAGAAAGGCTCTCTGATTTGCTCTGCGCTCATGCACTGTGACCCAGTGAAGAGCAG 1360
QY	521 AGTCTTTGGTGTGTTTCATGGTAGCCACTTATGGTGTGAGCGCAACTGCAACTGCTG 580
DB	1417 CACCGCGGAAGGCTACTTTTGGTTGCAATTTGGCTGCCCATGCAGCTGAACCTAGTGAAGCAG 1476
QY	640 AGACACTTGGCATTTTTCATGGTGGCACTTACGGGATGGAGAGCGCAACTGATAATGCTG 699
DB	1361 AGAGATTGGCTTTTGTGTCATCACCTCTGGGAAAGNATGAGTATTCAAAATGGGTAGTTG 1420
QY	581 CGAGATTTTACAAATGGTTCACCTCAGGAAATCAAGAGGGGAGAGTGGCTTCAGCAACTAA 640
DB	1477 AAAAGCTCAGGTTCTTGGCATCTCCTCAGGCGAAGATGAGTATTCATGGAATTTGAG 1536
QY	700 CAAGGTTTACAAAGTGGTTCACCTGAGGAGCAAGAACGGGTGCATGGTTCAGAACTTA 759
DB	1421 GAAGTCAGAGGAGTCTTTTGGAGATCATGCGCCGAGTTTCCATCAGCAAAAACCCCTCTTTG 1480
QY	641 CTTATGGTGTGTTTGGTGGTAAACGCTCAATACAGCAATTTCAACAGATCGCGGTAG 700
DB	1481 GTGTGTTCTTTCTGCACTGAGCCCTCGCTTACCGCTCGATCTATTTCTATCTCATTCCT 1540
QY	760 GCTATGGCGTGTGTCCTGGGTAAATCGCCAAATATGAACACTTTAAACAAGATTGGGAAG 819
DB	1537 TAAGTCAAGAAAGTCTTATTGAAGTAATGCTGAGTTTCATCGGCAAGAGCTCCCTTTG 1596
QY	701 ATGTGGATGAGCAACTCGGTAAACAAGGTGCAAGCGCATTTGTTCAAGTGGGCTCGGTG 760
DB	1541 CTCCTAAGTTTCTCCCTCAAGAAATTCATGTCAGCGTGTCTTTAGTATATGTTCAAGGCC 1600
QY	820 TGATAGTGAACAAATTGAGTGAACAAGGTGCAAAAAGTCTTTGCTGTGGCTTTGGTG 879
DB	1549 GTGTATTTCTTGCAGCAGTTCGCCCTCGTTTACAGCTCGCTACTATTCAATCTCATCAT 1656
QY	761 ACATGATCAATGCAATTTGAAGATGATTTTACTGCTTTGGCGAGAAATTTGTTGTGACTGAAT 820
DB	1557 GTGTATTTCTTGCAGCAGTTCGCCCTCGTTTACAGCTCGCTACTATTCAATCTCATCAT 1656
QY	880 ATGATGATCAGTGCATTTGAAGATGATTTTTCCTCGCTGGCGAGAACAGCTGTGSCAGAAAT 939
DB	1559 GTGTATTTCTTGCAGCAGTTCGCCCTCGTTTACAGCTCGCTACTATTCAATCTCATCAT 1656
QY	821 TGGATCAGTTGCTCAAGATGAGGATGCTGCTCCCTCAGTGGCTACACCGTATATTGCTA 880
DB	1597 GTGTATTTCTTGCAGCAGTTCGCCCTCGTTTACAGCTCGCTACTATTCAATCTCATCAT 1656
QY	940 TGGATCAAAATCTTTAGAGACGAGGATGATGCAAAATTTCTGCTGGCGAGAACAGCTGTGSCAGAAAT 999
DB	1601 CTACCGGAAGGTTCAACCGAGGAGTGTGTTCCACATGGAATGAAGCATGCAGTTCCTCAGG 1660
QY	881 CTCCTTCTGAAACAGGATGATTTTCAAGCAAACTGAGTTCCTCAGGAGGAGGCTGAT 940
DB	1657 CTCCTCGATTTGCACCGCTAGAGTCCATGTAACCTGTGCACCTAGTCTATGGTCCAACCTC 1716
QY	941 ACATAAATACTGCTAACCGCGATGTTGCTATTTGATATTTCTCCATCTTGCAGAACCAATTG 1000
DB	1661 A-----TAGCTGGGCTCTATTTTTTGTTCGAAACGTCGCTCAACTTTGGCCAGCAG 1705
QY	1000 CAATCTCTGAAATCGTTTGGTTATCCATGATACCACTAT---GAGTCTTGGAGATAAGC 1056
DB	1660 CTACCGGAAGGTTCAACCGAGGAGTGTGTTCCACATGGAATGAAGCATGCAGTTCCTCAGG 1660
QY	941 ACATAAATACTGCTAACCGCGATGTTGCTATTTGATATTTCTCCATCTTGCAGAACCAATTG 1000
DB	1661 A-----TAGCTGGGCTCTATTTTTTGTTCGAAACGTCGCTCAACTTTGGCCAGCAG 1705
QY	1057 ATCGAGCATGGCTAATGGGAATACCAATATGATATCCACCACTGCAAGTCAATG 1116
DB	1660 CTACCGGAAGGTTCAACCGAGGAGTGTGTTCCACATGGAATGAAGCATGCAGTTCCTCAGG 1660
QY	1001 TTGCTCAAAAGAGAGCTCCAAACCCAAAGTCTGATGATGATCTGATATCATCTCGAGT 1060
DB	1660 CTACCGGAAGGTTCAACCGAGGAGTGTGTTCCACATGGAATGAAGCATGCAGTTCCTCAGG 1660
QY	1117 TGGCTGTTCAGAGAGAGCTTTCACACACCCGAGTCTGATCGCTCATGTATATACACTTGGAGT 1176
DB	1660 CTACCGGAAGGTTCAACCGAGGAGTGTGTTCCACATGGAATGAAGCATGCAGTTCCTCAGG 1660
QY	1061 TCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATGTTGGTGTATTATGCTG 1120

DB	1177 TTGATATATCTGGCACTGGGATTTCTATGAAACAGGAGATCATGTGGGTGTTATGCTG 1236
QY	1121 AGAAGTGGCGATGAAACTGTGCGAGGAAGCAGGAAAGCTGTGGGTCAACCCCTGGATTGC 1180
DB	1237 AAAATCTCTGAAGATACTGTGTAGGAAGCTGCGAGATTGTGGGGCAGTCATTAGACTTGA 1296
QY	1181 TGTTCCTGATTCACACGGATAAAGAAAGAGCGGTCAACCCAGGGAAGCTCATTTACCACTC 1240
DB	1297 TATTCCTCTATTATACCGCAAGAGGAGATGGTACAGCTGAGAGGAGCTGTTACCCCCAC 1356
QY	1241 CTTTCCAGGTCTCTTGACCTTTACGATCTGCGCTTAGCAGCGCTATGCTGATCTTTTGAATC 1300
DB	1357 CTTTTCCTGGTCCCTGCACTCTACGTGCTGCACTGCTTGTATTATGAGATCTTCGAATC 1416
QY	1301 CTCCTAGAAAGGCTCTCTGATTTGCTCTGCGCTCATGCACTGTGACCCAGTGAAGAGCAG 1360
DB	1417 CACCGCGGAAGGCTACTTTTGGTTGCAATTTGGCTGCCCATGCAGCTGAACCTAGTGAAGCAG 1476
QY	1361 AGAGATTGGCTTTTGTGTCATCACCTCTGGGAAAGNATGAGTATTCAAAATGGGTAGTTG 1420
DB	1477 AAAAGCTCAGGTTCTTGGCATCTCCTCAGGCGAAGATGAGTATTCATGGAATTTGAG 1536
QY	1421 GAAGTCAGAGGAGTCTTTTGGAGATCATGCGCCGAGTTTCCATCAGCAAAAACCCCTCTTTG 1480
DB	1537 TAAGTCAAGAAAGTCTTATTGAAGTAATGCTGAGTTTCATCGGCAAGAGCTCCCTTTG 1596
QY	1481 GTGTGTTCTTTCTGCACTGAGCCCTCGCTTACCGCTCGATCTATTTCTATCTCATTCCT 1540
DB	1597 GTGTATTTCTTGCAGCAGTTCGCCCTCGTTTACAGCTCGCTACTATTCAATCTCATCAT 1656
QY	1541 CTCCTAAGTTTCTCCCTCAAGAAATTCATGTCAGCGTGTCTTTAGTATATGTTCAAGGCC 1600
DB	1657 CTCCTCGATTTGCACCGCTAGAGTCCATGTAACCTGTGCACCTAGTCTATGGTCCAACCTC 1716
QY	1601 CTACCGGAAGGTTCAACCGAGGAGTGTGTTCCACATGGAATGAAGCATGCAGTTCCTCAGG 1660
DB	1717 CCAGTGGCGAATTCATAAAGAGAGTGTGTTCAACTTGGATGAAGAGTGCAGTACCTTCGG 1776
QY	1661 A-----TAGCTGGGCTCTATTTTTTGTTCGAAACGTCGCTCAACTTTCAAGTTAC 1705
DB	1777 AGAAAGTCACAATTTGCAGCTCTGCTCCCAATTTTCATTAGGCGCATCTAATTTCAAAATTAC 1836
QY	1706 CAGCTGACCCCTCAACTCCAATTTATCATGCTGGGACCTGCTACAGGTTAGCTCTTTTCA 1765
DB	1837 CAGCCGACCCCTCAATTTCCAATTTGTCATGGTGGGCTCGGACCTGGTTTGGCCAACTTCA 1896
QY	1766 GAGGATTTCTGCAAGAAAGAAATGGCCCTCAAGGAAATGGTGTCTCAACTTTGGCCAGCAG 1825
DB	1897 GGGGATTCCTGCAAGAAAGAGCAGCAGCATTGAAGGAAGATGCGCTCAACTTTGGTCTGCTT 1956
QY	1826 TGCCTCTTTTTCGGATGTAGGAATCGTAATATGGAATTTTCACTTTTATGAAGAGCACTAAACA 1885
DB	1957 TACTGTTTTCGGTGTAGGAATCGTAGAATGGACTTTTATTTATGAGGAAGAGCTTTCAGA 2016
QY	1886 ACTTCGTGAAACGAGGAGTCAATTCGGAGCTAGTATTTCGCTTTTCACGTGAAGGGGAAA 1945
DB	2017 GTTTTGTGATCAAGGTGTAATATCAGAGCTGATTTATTCATTTTCAAGGAAGGGTTCAC 2076
QY	1946 AGAAGGAATATGTTTCAACATAAGATGATGGAGAAAGCAACGGATGTATGGAATGTGATAT 2005
DB	2077 AGAAGAGTATGTTTCAACACAAATGATGGAAGAAAGCTTCCCATGTTTGGAGTTAATCT 2136
QY	2006 CAGGGGACGGTTATCTCTATGTGTGGTGTGTCGCAAGGAATGGCCAGAGATGTCATC 2065
DB	2137 CTCAGGAGGGAATCTATATGTATGTGGGATGCTAAAGGGATGGCCAGAGACTGATCATC 2196
QY	2066 GCAGTTTGCATACCACTTCCCAAGAACAGGACCCCATGGAATCATCTGCTGCCGAAGCTG 2125
DB	2197 GTACACTCCATACCATAGTCCAGGACGAGGAATCGCGACTCATCTCAAGAGAGAGGCTG 2256
QY	2126 CAGTAAAGAAACTCCAAAGTTGAAGACGATATCTTAAGAGATGTCTCGGTGAT 2176

Db 2257 TTGTAAAGAACTCCAAATGGATGGAAGATATCTCAGGGATGTGTGGTAAT 2307

RESULT 8
AY596976
LOCUS
DEFINITION
Centaurium erythraea NADPH:cytochrome P450-reductase mRNA, complete cds.
ACCESSION
AY596976.1 GI:46403206
VERSION
AY596976.1
KEYWORDS
Centaurium erythraea
SOURCE
Centaurium erythraea
ORGANISM
Centaurium erythraea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Gentianaceae; Centaurium.
1 (bases 1 to 2079)
Schwarz, H. and Beerhues, L.
Molecular cloning of NADPH:cytochrome P450-reductase from Centaurium erythraea cell cultures
Unpublished
2 (bases 1 to 2079)
Schwarz, H. and Beerhues, L.
Direct Submission
Submitted (08-APR-2004) Institut fuer Pharmazeutische Biologie, Universitaet Braunschweig, Mendelssohnstrasse 1, Braunschweig 38106, Germany
Location/Qualifiers
1..2079
/organism="Centaurium erythraea"
/mol_type="mRNA"
/isolation_source="cell culture"
/db_xref="taxon:172057"
1..2079
/codon_start=1
/product="NADPH:cytochrome P450-reductase"
/protein_id="AA592623.1"
/db_xref="GI:46403207"
/translation="METKLELVRSIESALGVSLGEDGDKVILVLTSLAVIGLVVF
LWKSRRSRETSVVVPLKLTALQEESEVDLDPSKVTVFFGTGTGAEFPAKAL
AEIKTRYEKAVVVDLDYDAADDOYBEKLEKLETLAFMWATYGGSEFTNAAIFY
KWFSEKREPELQOITYGVFGNDRQYEHFNKIGVDDQLEQAKKIVPLGLGD
QCIEDFSAWRDQLMPELDKILLEDSSAAVATPYTAATHEYVIVHDSADSYSHK
OLNMNNGNTSYDQHPLNVNAVORELHTPESDRSCITHEFLIAGTGIKYETGDHVG
YANECNVEEARLLQSLDLTFSIHADKEDCTPLGSLAPFPSPCTLRALARYA
DLTPPKTALIALAHSSEPSAEERLKLSSQQGDDYSQWIVGSRSLLEWMAFP
SAPPLGVFFAPLRLQRYISISSPFPVNRHVTCALVYGPPTGRIRHGVCS
WMKNVPSERSHDSQAPVFIPTSNFKLPADPISPIVMIGPGLAPFRGFLQERFVL
KEEGAQLGALLPFGCRNRMDFIYESLKKYDEGVSELIVAFSREGPQKEYVQHK
MMEKAAEIVSLISQEGLYVCGDKGMARDVHRALHTIVQEQEKDTSKAEIVKQLQ
MNGRYLRDVM"

CDs

FEATURES
source
1..2079
/organism="Centaurium erythraea"
/mol_type="mRNA"
/isolation_source="cell culture"
/db_xref="taxon:172057"
1..2079
/codon_start=1
/product="NADPH:cytochrome P450-reductase"
/protein_id="AA592623.1"
/db_xref="GI:46403207"
/translation="METKLELVRSIESALGVSLGEDGDKVILVLTSLAVIGLVVF
LWKSRRSRETSVVVPLKLTALQEESEVDLDPSKVTVFFGTGTGAEFPAKAL
AEIKTRYEKAVVVDLDYDAADDOYBEKLEKLETLAFMWATYGGSEFTNAAIFY
KWFSEKREPELQOITYGVFGNDRQYEHFNKIGVDDQLEQAKKIVPLGLGD
QCIEDFSAWRDQLMPELDKILLEDSSAAVATPYTAATHEYVIVHDSADSYSHK
OLNMNNGNTSYDQHPLNVNAVORELHTPESDRSCITHEFLIAGTGIKYETGDHVG
YANECNVEEARLLQSLDLTFSIHADKEDCTPLGSLAPFPSPCTLRALARYA
DLTPPKTALIALAHSSEPSAEERLKLSSQQGDDYSQWIVGSRSLLEWMAFP
SAPPLGVFFAPLRLQRYISISSPFPVNRHVTCALVYGPPTGRIRHGVCS
WMKNVPSERSHDSQAPVFIPTSNFKLPADPISPIVMIGPGLAPFRGFLQERFVL
KEEGAQLGALLPFGCRNRMDFIYESLKKYDEGVSELIVAFSREGPQKEYVQHK
MMEKAAEIVSLISQEGLYVCGDKGMARDVHRALHTIVQEQEKDTSKAEIVKQLQ
MNGRYLRDVM"

ORIGIN

Query Match 39.2%; Score 1039; DB 8; Length 2079;
Best Local Similarity 72.7%; Pred. No. 1e-233;
Matches 1361; Conservative 0; Mismatches 495; Indels 15; Gaps 1;

QY 320 AAGAAGAGGAGGATGAAGTTGATCCCTGGTAAATTAAGCTCACTATATTTTGGTA 379
DB 209 AGGAGGAGGAGGAGGAGGATTTGGATCCCTAGCAAGTTAAGGTACCGTGTGTTTGGTA 268
QY 380 CTGAGACTGCTACTGCTGAAGGATTTGCTAAGGCATTGGCAGAGAAATTAAGCAAGT 439
DB 269 CACAGACTGGACTGCTGAGGGTTTGTCTAAGGCATTGGCAGAGAGATCAAGCAAGAT 328
QY 440 ACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCCGAGGATGATCAAT 499
DB 329 ATGAGAAAGCAGTTGTTAAAGTAGTTGATTTGGATGATTATGCTGCTGATGATGACCAAT 388
QY 500 ATGAGAGAAATTAAGAAAGAGTCTTTGGTGTGTTTTTCATGGTAGCCACTTATGGTGATG 559
DB 389 ATGAGGAAAAATTAAGAAAGAGACCTTGGCAATTTTTCATGTTGGTGGCCACTTATGGTGATG 448

QY 560 GTGAGCAACTGCAACTGCTGCAGATTTTACAAATGGTTCTACTCAGAAACATGAAAGGG 619
DB 449 GAGAGCAACTGATATATGCTGCTCGGTTTACAAATGGTTTTCGAGGTTAAAGAAAGGG 508
QY 620 GAGAGTGGCTTCAGCAACTAATATATGTTGTTTGGTTGGGTAAACCGTCAATACGAGC 679
DB 509 AGCCCTGGCTTCAGCAACTTACATATGGGGTTTTTGGTTTGGGAAACCGTCAATATGAAC 568
QY 680 ATTTCAACAGATCGCGGTAGATGTGGATGAGCAACTCGGTAAACAGGTGCAAGCGCA 739
DB 569 ATTTCAATAGATTTGGGAAGGTGATCGATGACCAACTTATTTGAACAGGTGCAAGGA 628
QY 740 TTCTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTGGC 799
DB 629 TTGTACCACTTGTCTTGGTGATGATGACCAATGATTTAGGATGATTTTCTGCTTGA 688
QY 800 GAGATTTGTGGATGCAATTTGGATGATGCTCAAGATGAGGATGCTGCTCTTTCAG 859
DB 689 GAGATCAACTTTGGCCAGAACTTGAATAAATCTTTTGGATGAGGATAGTTTCAGCTGCTG 748
QY 860 TGGCTACACCGTATATTTGCTTCTTCAATACAGGGTGTGATTCAGAAACTACGG 919
DB 749 TAGCCACCCCTATCTCTGCAATTCATGAGTATCGGGTTGTGATCCCATGATCTTCTG 808
QY 920 TCGCGCTCTGATGATGATAACACATATACTGCTAACCGCGATGTTGCAATTTGATATTC 979
DB 809 CTGATTTTATGACATAGCAATTCGACATGATGATGATGATGATGATGATGATGATTC 868
QY 980 TCATCTCTTGCAGAACCATTTGTTGCTCAACAAAGAGAGCTCCACAAACCCAGCTGATA 1039
DB 869 AACACCATGCTAGTCAATGTTGCTGTTTCAGAGGAGCTCCACACACCTGATCAGATC 928
QY 1040 GATCTGTATACATCTGGAGTTCGACATATCAGGCTCTTCCCTTATATATGACACTGGAG 1099
DB 929 GCTCATGCAATTTTGAATTTGATATAGTGGCACAGAAATTAATAATGAAACTGGAG 988
QY 1100 ATCATGCTGGTGTATATGCTGAGAACTGCGATGAAACTGTCGAGGAGGAGGAGGAGCTGT 1159
DB 989 ATCAGTGGGTGTATATGCTGAGAAATTTGAGAGAAATTTGAGAGAGCTGCAAGATTGT 1048
QY 1160 TGGGTCAACCCCTGGATTTGCTGTTTCAATTCACCGGATCAAGAGAGCGGTGCAACCC 1219
DB 1049 TGGGTCAATCTTTAGACTTGAATTTTCAATCCATGCTGACAAAGAGGATGGCACACCT 1108
QY 1220 AGGAGCTCATATACACCTCTCTTCCAGGTCTTTCACCTTACCATCTGCTCCCTAGCAC 1279
DB 1109 TGGGAGGCTCATTTGGCTCTCTCTTCCAGGGCTTTCACACCTTCGAACTGCACTTGTCT 1168
QY 1280 GCTATGCTGATCTTTTGAATCTCTTAGAAAGGCTTCTCTGATTGCTCTGCTCGCTCATG 1339
DB 1169 GTTATGCTGATCTTTAACTCTCTCCCAAAAGACAGCTTTGATTGCTTTAGCTGCTCAT 1228
QY 1340 CATCTGTACCCAGTGAAGCAGAGATTCGGCTTTTGTTCATCACTCTTGGGAAAGATG 1399
DB 1229 CAAGTGAACCAAGCGAAGCAGAAAGGCTAAATTTCTATCATCTCAGCAGGAAAGATG 1288
QY 1400 AGTATTTCAAAATGGGTAGTTGGAGTCAGAGGATCTTTTGGAGATCATGGCCGAGTTTC 1459
DB 1289 ATTTATCAAAATGGATCGTGGGAAGTCAGAGAGTCTCTCTTGAAGTTATGGCTGAAATTC 1348
QY 1460 CATCAGAAAAACCCCTCTTGTGTGTCTTGTGCTGAGTACCCCTCGCTTACCCGCTC 1519
DB 1349 CTTTCAGAAAAACCTCTCTTGGCGTATTTTTCAGCTATAGCACCTCAATATACAGCCCC 1408
QY 1520 GATATCTTATCTCATCT 1579
DB 1409 GTTACTACTCTATCT 1468
QY 1580 CTTTAGTATATGTTCAAGCCCTACCGGAGGGTTCACCGAGGATGTTTTCGACATGGA 1639
DB 1469 CGCTAGTTTATGGGCT 1528
QY 1640 TGAAGCATCAGTTCC-----TCAGGATAGCTGGGCTCCTATTTTGTTC 1684

Db	1529	TGAAGATGAGTTCCATCAGAAAGGAGCCATGATCTAGCCAGGCGCTGTTTTATCA	1588		
Qy	1685	GAACGTCAAACCTTCAAGTTACCAAGTGAACCCCTCAACTCCAATATCATGGTGGGACCTG	1744		
Db	1589	GGACATCAAATTTCAAATTTACCAAGTGAATCTTTCCATTCCTCAATGTTATGATAGGACCTG	1648		
Qy	1745	GTACAGGTTAGTCTCTTTTCAGAGGATTTCTGCAGGAAGAATGGCCCTCAAGGAAATG	1804		
Db	1649	GAACCGGCTGGCTCCATTTAGAGGATCTTACAGGAAAGATTTGTGCTGAAGGAAAGAG	1708		
Qy	1805	GTGCTCAACTTGCGCCAGCAGTCTCTTTTTCGGATGTAGGAATCGTAAATATGGACTTCA	1864		
Db	1709	GTGCTCAACTTGCTCTGCTCTATTGTTCTTTGGTTAGAAATCGCAGAAATGGAATTTCA	1768		
Qy	1865	TTTATGAAGACGAACTAAACAACCTTCGTGGAAACGAGAGTCATTTCCGAGCTAGTTATTG	1924		
Db	1769	TTTATGAGAGCGAGTTTGAAAAAATATCAGGATGAAGGTGTAGTATCCGAGTTGATAGTTG	1828		
Qy	1925	CTTTTTCAGTGAAGGGGAAAAAGAGGAATATGTTCAACATAAGATGATCGAGAAAGCAA	1984		
Db	1829	CATTTTCAAGGGAGGGCCACAGAAAGATATGTCAACATAAGATGATGGAAGAGCAG	1888		
Qy	1985	CGCATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTGATGCCAAGG	2044		
Db	1889	CCGAATCTGGAGTTTGCTCTCCAGAGGGGTATCTTTACGTATGTGGAGATGCTAAGG	1948		
Qy	2045	GAATGCCAGAGATGTCATTCGCACGTTGCATACCATTTGCCAAGAACAGGACCCATGG	2104		
Db	1949	GTATGCCAAGAGACGTTTCATCGTGTCTTCATACCATTTGTTCAAGAGCAGGAAAGACGG	2008		
Qy	2105	AATCATCTGTCGCGAAGCTGCAGTAAAGAAACTCCAAAGTTGAAGAACGATATCTAAGAG	2164		
Db	2009	ATTCTTCAAGGGCGGAGGCTATCGTGAACAGCTACAGATGAATGGGCGGTATCTAAGG	2068		
Qy	2165	ATGTCGTGGTGA	2175		
Db	2069	ATGTTTGGTGA	2079		
RESULT 9	AY520902	2059 bp	mRNA	linear	PLN 01-FEB-2004
LOCUS	Hypericum androsaemum NADPH:cytochrome P450-reductase mRNA,				
DEFINITION	complete cds.				
ACCESSION	AY520902				
VERSION	AY520902.1	GI:41350272			
KEYWORDS	Hypericum androsaemum				
SOURCE	Hypericum androsaemum				
ORGANISM	Hypericum androsaemum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
TITLE	rosids; eurosids I; Malpighiales; Clusiaceae; Hypericum.				
JOURNAL	1 (bases 1 to 2059)				
REFERENCE	Schwarz,H. and Beerhues,L.				
AUTHORS	Molecular cloning of NADPH:cytochrome P450-reductase from Hypericum				
TITLE	androsaemum cell cultures				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 2059)				
AUTHORS	Schwarz,H. and Beerhues,L.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-JAN-2004) Institut fuer Pharmazeutische Biologie,				
REFERENCE	Universitaet Braunschweig, Mendelssohnstrasse 1, Braunschweig				
AUTHORS	38106, Germany				
TITLE	Location/Qualifiers				
SOURCE	1..2059				
	/organism="Hypericum androsaemum"				
	/mol_type="mRNA"				
	/db_xref="taxon:140968"				
CDS	1..2058				
	/function="catalyzes the reduction of cytochrome P450"				
	/codon_start=1				
	/product="NADPH:cytochrome P450-reductase"				

		protein_id="AAS00459.1"	
		/db_xref="GI:41350273"	
		/translation="MSSSGSEVWVWALGVGTDSLVIVITTSIVAVGVVVALFLWKRSS	
		DRGDKPRTLVPKPLSLKEEEDAEKTKVICFYGTQGTAGFAKALAEIKVR	
		YKAVKVVLDLDDDDOYBEHKLKETLAFWVATYGDGPTDNGAARFYKWFTEH	
		ERGVMLQQLKFGVFLGNROYEHFNKI AKVLEOFCEQAKRLIPVGLGDDQCI EDD	
		FTAWRELLPELDPILLRDEDNANAASPTPTAAILSYRVVVIHDPPTLISVEDKPA	
		NATFPAQHPVRNVAVARELHKPESDRSCIHLELDISGTGRIYEGADHGVYTENCAE	
		NYEEAGRLGQPLDLVFSYTEKEDEGTPLGGSPFPFPGCTLOQTSLAARFPAIPLG	
		KAALLAALAHASEPSEARLKLASPOGQDEYAVWVTSQRSLSEYFVMSNMKNVLS	
		IFFAVAPRLOPRYYSISSPRYAPHRVHVTCALVYGPPTGRIRHGVCSNMKNVLS	
		LERSSDCSNAPYIIRPSNFKLPANPSTITMVGPGTGPAPFRGFLQERMALEDGVQL	
		GALLLPFCGRNRMQDIYEEELNFFVEQALSELIVASREGEFKDYVQKHQMDKAA	
		IVEVLSQGAHHYVCGDAKWARDVHRTLHTIVQEQNLDSKTELFVFKLQMDGRYLR	
		NVM"	
ORIGIN			
	Query Match	38.9%;	Score 1030.8; DB 8; Length 2059;
	Best Local Similarity	72.4%;	Pred. No. 8.8e-232;
	Matches 1357;	Conservative 0;	Mismatches 502; Indels 15; Gaps 1;
QY	318	TAAAGAAGAAGAGGAGATTGAAGTTGATCCTCGTAAAAATTAAGCTCACATATATTTTGG	377
Db	186	TAAGGAGGAGGAGGAGGAGACGAGCCCGAGGGAGACCAAGGCTCTGCACTCTTCA	245
QY	378	TACTCAGACTGTGATCTGCTGAAGGATTTGCTTAAGGCATTTGGCAGAGAAGAAATTAAGGCAAA	437
Db	246	CACCCAGACCGGCATCTGCCGAGGGATTCGCCAAGGCTTTGGCTGAGGAGATCAAGGTTG	305
QY	438	GTACAAGAAGACAGTTGTTAAAGTAGTTCACCTGGATGACTATGCAGCCGAGGATGATCA	497
Db	306	ATATGAAAAGCAGTGTCAAAGTTGTTGACTTTGGATGATTTATGCTTTGGATGATGATCA	365
QY	498	ATATGAAGAAGAAATTAAGAAGAGTCTTTTGGTGTGTTTTTTCATGGTAGCCACTTATGGTGA	557
Db	366	ATATGAAGAAGAGCTGAAAAAGGAGACCTTTGGCTTTTTCATGGTGGCCACGATGGGA	425
QY	558	TGGTAGCCCAACTGACAAATGCTGCGAGATTTTACAAATGGTTTCACTCAGAACATGAAG	617
Db	426	TGGAGAACCTACTGATGAACGAGCCCGGATTTTACAAAGTGGTTTCACTGAGGAACATGAAG	485
QY	618	GGGAGAGTGGCTTTCAGCAACTAACTTATGGTGTGTTTTGGTGTGTTGGGTAAACCGTCAATACGA	677
Db	486	GGAGTCTGGCTTCAACAACCTCAATTTGGTGTATTCGGTCTTTGGTAATCGCCNATATGA	545
QY	678	GCATTTCAAAGAAGTCGGGTAGATGTGGATGAGCAACTCGGTAAACAAGGTGCAAAAGCG	737
Db	546	ACATTTCAAAGAAGTAGCTAAGGTGCTTGTGATGAACAAATCTCTGTGAACAAGGAGCTAAGCG	605
QY	738	CATTGTTCAAGTGGGGCTGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTTG	797
Db	606	CCTCATTCCTGTGGGCTCGGTGATGATCAGTGCATTTGAGGATGATTTTCACTGCTTG	665
QY	798	GGGAGAAATTTGTGGACCTGAATTTGATCAGTTGCTCAAGATGAGGATGCTGCTCTTC	857
Db	666	GAGAGAAATTTATGGCTTGAGCTGATCCATTTCTAAGAGATGAAGATTAATGCGAATGC	725
QY	858	AGTGGCTACACCGTATATTGCTACTGTTCTCTGAATACAGGGTAGTGATTTACGAAACTAC	917
Db	726	TGCATCTACACCATACACTGCAGCTATATCTTGAATATCGTGTGTTTATTTCATGATCAAC	785
QY	918	GGTGGGGCTCTGGATGATAACACATAAATACTGCTAAGCGGATGTTTGCATTTCATAT	977
Db	786	GACGCTATCAGTCGAGGATTAAGTTTTCGAAATTTGGCGAAACGGGAATGCAACTTTTATGC	845
QY	978	TCTCCATCTTCGAGAAACCATTTGTTGCTCAACAAGAGAGAGCTCCCAAAACCCCAAGTCTGA	1037
Db	846	TCAACATCCATGAGGGTTAATGTTGCTGTCCAGAGAGAGCTTCAACAGCCGAGTCTGA	905
QY	1038	TAGATCTCTGATATCTCTGGAGTTGACATATCAAGGCTCTTCCCTTACATATGAGACTGG	1097
Db	906	CCGGTATCATCATCATCTGGAATTTGACATATCAGGACTGTTGATTTAGATACGAAGCTGG	965

MMEKAAQVMDLKEEBGYLYVCGDAKGMARDVHRTLHTIIVQEGBVSSSEAEALVKKLQ
TEGYLRDWN"

ORIGIN		Query Match		37.6%; Score 997.2; DB 8; Length 2340;	
		Best Local Similarity		71.4%; Pred. No. 7.2e-224;	
		Matches 1349; Conservative		0; Mismatches 523; Indels 18; Gaps 2;	
Qy	310	ATAATTGATGAAGAAGAGGAGATTGAAGTTGATCTCTGGTAAAAATTAAAGCTCACTATA	369.		
Db	291	ATGGCTAAGCAGCAGGATGATGATTGGATTGGGATCCGGGAAGACTAGAGTCTCTATC	350		
Qy	370	TTTTTTGGTACTCAGACTGCTACTGCTGAAGGATTTGCTTAAGGCATTGGCAGAGAATTT	429		
Db	351	TTCTTCGGTACGGCAGCTGGAACAGCTGAGGGATTTGCTAAGGCATTTATCCGAAGAAATC	410		
Qy	430	AAGCCAAAGTACAAGAAGCAGTTGTTTAAAGTAGTTGACCTGGATGACTATGACGGCAG	489		
Db	411	AAAGCGGATATGAAAGAAGCAGCAGTCAAGTCAATTGACTTGGTGAATGCTGCGGAT	470		
Qy	490	GATGATCAATATGAAGAGAAATTAAGAAGAGATCTTTGGTGTTTTTCATGGTAGCCACT	549		
Db	471	GATCACCAGTATGAAGAGAAATTAAGAAGAGAACTTTGGCAATTTTCTGTGTGCTACT	530		
Qy	550	TATGGTGTGCTGAGCCCACTGACAACTGCTGCGAGATTTTACAATGCTTCACTCAGGA	609		
Db	531	TATGGAGATGGAGGCGCTACTGACAACTGCTGCGAGATTTTACAATGCTTACGGAGGA	590		
Qy	610	CATGAAGGGGAGAGTGGCTTTCAGCAACTAACTTATGGTGTTTTGGTGGGTAAACCGT	669		
Db	591	AATGAACGGGATATAAGCTTCAACACTAGCATATGGTGTGTTTGTCTTGGTAAATCGC	650		
Qy	670	CAATACGAGCATTTCAACAGATCGCGGTAGATGTGATGAGCAACTCGGTAAACAAGGT	729		
Db	651	CAATATGAACATTTAATAAGATCGGATAGTTCTTGATGAAGAGTTATGTGAAGAAAGGT	710		
Qy	730	GCAAGGCGATTTTCAAGTGGGCTCGGTGACGATGATCAATGCAATTGAGATGATTTT	789		
Db	711	GCAAGGCGTCTTATGAACTGCGTCTAGGAGATGATGATCAGAGCAATTGAGGATGATTT	770		
Qy	790	ACTGCTTGGCGAGAAATTTGTTGGACTGTAATGGATGGATCAGTTGCTCAAGATGAGGATGCT	849		
Db	771	AATGCCCTGGAAGAAATCACTATGTTCTGAGCTAGACAGCTCTCAAGACGAGGATGAT	830		
Qy	850	GCTCCTTCACTGAGTACACCGTATATTTGCTACTGTTCTCTGAAATACAGGGTAGTATCAC	909		
Db	831	AAAAAGT---GTGGCAACTCTTATACAGCTGTTATTCTCTGAAATACCGGGTGGTACTCAT	887		
Qy	910	GAACTACGCTCGGGCTCTGGATGATAAACAATATAACTGCTAAACGGCGATTTGCA	969		
Db	888	GATCCTCGGTTTCAACTCAAAATCAATGGAATCAAAATGGCCAAATGGAATACTACT	947		
Qy	970	TTTGATATTCCTCATCTCTGAGAACCATTTGTTGCTCAACAAAGAGAGACTCCCAAAACCC	1029		
Db	948	ATTGACATTCATCATCCTCGAGATTGATGTTGCTGTGAGAGAGGCTTCAACACAT	1007		
Qy	1030	AAGTCTGATAGATCTGTATACATCTGGAGTTGCAATATCAGGCTCTTCCCTTACATAT	1089		
Db	1008	GAATCTGATCGGCTTGGATTCATCTCAGTTCGACATATCCAGGACGGGTATTAATAT	1067		
Qy	1090	GAGACTGGAGATCATGTTGGTGTATTATGCTGAGAACTGCGATGAACTGTCGAGGAGCA	1149		
Db	1068	GAAACAGGTACCATGTAGGTGTATATGCTGAAATTCATGTTGAAATAGTTTGAAGAAGCT	1127		
Qy	1150	GGGAAGCTGTGGGTCAACCCCTGGATTTTGTCTGTTTCAATTCACACGGATAAAGAAGAC	1209		
Db	1128	GGAAATTTGCTGGCCACTCTTTAGATTAGTATTTTCCATACATGCTGACAGGAGAT	1187		
Qy	1210	GGGTCAACCCGAGGAGCTCATTAACACCTCTTTTCCAGGTCCTTTCACCTTACGATCT	1269		
Db	1188	GGCTCCCAATTGGAAGCGCAGTGCGGCTCTCTTCCCTGCTGCTCATGACACTTGGACT	1247		
Qy	1270	GCCTTAGCAGCTATGCTGATCTTTTGAATCTCTTGAAGAGGCTTCTGATGCTCTG	1329		

Db	1248	GGTTTGGCAAGATACGACAGCCTTTTGAACCTCTCTCGAAAGTCTCGGTAGTTGCTTG	1307		
Qy	1330	TCGGCTCATGTCATCTGTACCCAGTGAAGCAGAGAGATTCCGCTTTTGTTCATCACCTCTG	1389		
Db	1308	GGGGCTATGCCACTGAACCAAGTGAAGCCGAGAACTTTAAGCACCTGACATCACCTGAT	1367		
Qy	1390	GGAAAGATGAGTATTTCAAAATGGGTAGTTGGAAAGTCAAGGAGTCTTTTGGAGATCATG	1449		
Db	1368	GGAAAGGATGAGTACTCTCAATGGATTGTTGCAAGTCAAGAGTCTTTTAGAGGTGATG	1427		
Qy	1450	GGCGAGTTTCCATCAGCAAAACCCCTCTTGTGTGTTCTTCTGCTGACGTAGCCCTCGC	1509		
Db	1428	GCTGCTTTTCCATCTGCAAAACCCCACTAGGTGATTTTGTGCAATAGTCTCTCGT	1487		
Qy	1510	TTACGCCCTCGATATCTATTCTATCTCATCTCTCTTAAGTCTTCTCCCTCAAGAAATTCAT	1569		
Db	1488	CTACAACTCTGTTACTTACTCTCATCTCTCGCAAGATTGGCGCAAGTAGAGTTTCAAT	1547		
Qy	1570	GTGACGTGTCTTTTAGTATATGCTCAAGCCCTACCGGAAGGTTTCCCGAGGAGTGTGT	1629		
Db	1548	GTTCATCCGCACTAGTATATGCTCCACTCTCTCTGCTAGAAATCCACAAGGGTGTGTGT	1607		
Qy	1630	TCGACATGATCAAGCATCGACTGCTCTCAGGA-----TAGCTGGGCTCCT	1674		
Db	1608	TCTACGTGATGAAGATGCAAGTCTCTCGGAGAAAGTCATGAATGTAGTGGAGCCCA	1667		
Qy	1675	ATTTTGTTCGAAACGTCAAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTAATCATG	1734		
Db	1668	ATCTTTATTCGAGCATCTAATTTCAAGTTACCATCCAACCTTCAACTCCAATCGTTATG	1727		
Qy	1735	GTGGACCTGGTACAGGGTTAGCTCTTTTCAAGAGATTTCTGAGGAAAGATGGCCCTC	1794		
Db	1728	GTGGACCTGGGACTGGGCTGGCACCTTTTAGAGGTCTTCTGAGGAAAGATGGCACTA	1787		
Qy	1795	AAGGAAATGGTGTCTCAACTTCGCCAGCAGTCTCTTTTTCGGATGTAGGAATCCGTAAT	1854		
Db	1788	AAAGAAATGGGAGAGAACTAGGTTTCATCTTGTCTCTTTTGGGTGTAGAAATCGACAG	1847		
Qy	1855	ATGGACTTCATTTATGAAGACGAATTAACAACACTTCGTGGAACGAGGAGTCAATTCGGAG	1914		
Db	1848	ATGGACTTTATATACGAGGATGAGTCAATAATTTTGTGATCAAGGCGTAATATCTGAG	1907		
Qy	1915	CTAGTTATTTGCCCTTTTACGTGAAGGGGAAAGAGAAATATGTTCAACATTAAGATGATG	1974		
Db	1908	CTCATCATGGCATTTCTCCGCTGAAGGAGCTCAGAAGGAGTATGTTCAACATTAAGATGATG	1967		
Qy	1975	GAGAAAGCAACGATGATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGT	2034		
Db	1968	GAGAGGACGACAAAGTTTGGGATCTAATAAGGAAAGAGGATATCTCTATGTATCGGT	2027		
Qy	2035	GATGCCAAGGGAATGGCCAGAGATGTCCATCGCACGTCGTTCATACCAATTCGCCAAGAACAG	2094		
Db	2028	GATGCTAAGGSCATGSCGAGGGGACGTCACACCGAACTCTACACACCATTTGTTCAAGGAGCAG	2087		
Qy	2095	GGACCCATGGAATTCATCTGCTCGAGGCTGAGTAAAGAAACTCCAAGTTGAAGAACGA	2154		
Db	2088	GAAAGTGTGAGTTCTGTCAGAGGACAGGCTATAGTTAAGAAACTTCAAAACCGAAGGA	2147		
Qy	2155	TATCTAAGAGATGCTCTGGGTGATCGAATGTA	2184		
Db	2148	TACCTCAGAGATGCTCTGGGTGATTGATGATA	2177		

RESULT 11
BT008426
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BT008426
Arabidopsis thaliana At4g24520 gene, complete cds.
BT008426.1
GI:30725525
FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana

2079 bp
mRNA
linear
PLN 15-MAY-2003

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

1. (bases 1 to 2079)
Cheuk, R., Chen, H., Kim, C.-J., Shinn, P., Bowser, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Hsuan, V. W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.
Arabidopsis ORF clones
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS

2. (bases 1 to 2079)
Cheuk, R., Chen, H., Kim, C.-J., Shinn, P., Bowser, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Hsuan, V. W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.
Direct Submission

TITLE
JOURNAL

Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, POEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.-J., Shinn, P., Bowser, L., Chan, M. M., Chang, C. M., Dale, J. M., Hsuan, V. W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Miranda, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Southwick, A., Tang, C. C., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Davis, R. W., Theologis, A., and Ecker, J. R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES
source

Location/Qualifiers
1. .2079
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
/clone="U15655"
/ecotype="Columbia"
/notes="This clone is in pUNI 51"

CDS

1. .2079
/notes="NADPH-ferrihemoprotein reductase ATR1"
/codon_start=1
/product="At4g24520"
/protein_id="AAP37785.1"
/db_xref="GI:30725526"
translations="MTSALYASDLFKQLKSLMGTSLSDDVVLVIATSLALVAGFVV
LWKTTADRSGLKPLMTPKSLMAKEDDDLDLGSQKTRVSIFFQOTGTAEGRFPA
LSEIARVEKAVKVIDDDYAADDDQVEEKLKETLAFPCVATYGDGEPTDNRPF
YKFTSENERDKLQQLAYFALGNRQYEHFNKIGIVLDBELCKRGAKEFLVEGLGD
DSQIIEEDFNWAKESLWELDKDDKSNATPYAVIPEYRVTHDPFRFTQKSM
ESNVANGNTTIDIHPCRDVAVQKELHSDHESDRSCILHLEFDISRTGITYETGDHVG
YAEHVETIIEAGKGLGSLDLVFIHADKEDGPSLESAVPPFPGPCTLTGTGLRYA
DLNPKRKSALVALAAVATPESEAELKHLTSPDGKDEYSOMIVASORSILLEMAFP
SAKPLGVFAATAPLQPRYSISSPLASRVHTVSALYVGPFTPTGRHKGVCST
WMKNVPAEKSHCSGAPFIRASNFKLPNSPTPIVMVPGTGLAPFRFGLOERVAL
KEDGELGSLFLPFGRNQMDFIYEDLNLFNDQGVISELIMAFREGAQKEYVQHK
MMEKAAQVMDLIIKEEGLYVCGDKAGMDVHRTLTHITVQEBEGVSSSEAEATVKLQ
TEGRYLRDVM"

ORIGIN

Query Match 37.5%; Score 994.6; DB 8; Length 2079;
Best Local Similarity 71.5%; Pred. No. 3e-223; Indels 18; Gaps 2;
Matches 1344; Conservative 0; Mismatches 519;
QY 310 ATAAATGATAAAGAAGAAGAGGAGATTGAAGTTGATCTCTGGTAAAAATTAAGCTCATTATA 369
DB 202 ATGGCTAAGGACGAGGATGATGATTGGGATTTGGGATCCGGGAAGACTAGAGTCTCTATC 261
QY 370 TTTTGTGGTACTCAGACTGCTGCTGAAGGATTTGCTAAGGCATTGGCAGCAAGAAATTT 429
DB 262 TTCTTCGGTACGCAGACTGGAACAGCTGAGGATTTGCTAAGGCATTATCCGAAGAATC 321
QY 430 AAGGCAAAAGTCAAGAAGACAGTTGTTAAAGTAGTTGACCTGCATCACTATGACGCGAG 489
DB 322 AAGCAGATATGAANAAGCAGCAGTCAAGTCATTGACTTGGATGACATGCTGCGGAT 381
QY 490 GATGATCAATATCAAGAGAGAAATTTAAAGAAAGAGTCTTTGGTGTGTTTTCATGGTAGCCACT 549
DB 382 GATGACCAGTATCAAGAGAGAAATTTGAAGAAGGAAACTTTGSCATTTTCTGTGTGTACT 441
QY 550 TATGTGTGTTGAGGCAACTGCAATGCTGCGAGATTTTACAAATGGTTCACTCAGGAA 609
DB 442 TATGGAGATGAGAGGCTTACTGCAATGCTGCCAGATTTTACAAATGGTTTACGAGGAA 501
QY 610 CATGAAGGGGAGAGTGGCTTCAGCAACTAACTTATGTGTGTTTTCGTTGGTAAACCGT 669
DB 502 AATGAACGGGATATAAAGCTTCAACAACTAGATATGGTGTGTTGCTCTTGGTAATCGC 561
QY 670 CAATCAGACATTTCAACAAGATCGCGGTAGATGTGGATGAGCAACTCGGTAAACAAGGT 729
DB 562 CAATATGAACATTTAATAAGATCGGATAGTCTTGTATGAAGATATGTAAGAAAGGT 621
QY 730 GCAAGCGCATTTCAAGTGGGGTTCGGTGACGATGATCAATGCAATGCAAGATGATTTT 789
DB 622 GCAAGCGCTTATTGAAGTTCGGTCTAGGAGATGATGATCAGAGCATTCAGGATGATTTT 681
QY 790 ACTGCTTGGCGAGATTTGTTGGACTGAATTTGGATGAGTTCCTCAAGATGAGGATGCT 849
DB 682 AATGCTTGAAGAATCACTATGCTGAGCTAGACAAGCTCTCAAGACAGGATGAT 741
QY 850 GCTCTTCACTAGTGGCTACACCGTATATTTGCTACTGTTCTGAATACAGGGTAGTATTAC 909
DB 742 AAAAGT---GTGCAACTCTCTTATACAGCTGTTATTCTCTGAATACCGGGTGGTACTCAT 798
QY 910 GAAACTACCGTCCGGCTCTGGATGATAAACAATAAATACTGCTAACCGCGATGTTGCA 969
DB 799 GATCTCTCGGTTTACAACCTCAAAATCAATGGAATCAAAATGTGGCCAATGGAATACTACT 858
QY 970 TTTGATATTTCTCCATCTTGCAGAACCATTTGTTGCTCAACAAGACAGCTCCACAACCC 1029
DB 859 ATTGACATTCATCTCCCTGCGAGTTGATGTTGCTGTCAGAGAGGCTTTCACACAT 918
QY 1030 AAGTCTGATAGATCTCTGTATATACATCTGAGTTCGACATATCAGGCTCTTCCCTTACATAT 1089
DB 919 GAATCTGATCGGCTCTGCATTCATCTCGAGTTCGACATATCCAGGACGGGTATTACATAT 978
QY 1090 GAGACTGAGATCATGTTGGTGTATTGCTGAGAACTGCGATGAAACTGTGCGAGGAAGCA 1149
DB 979 GAAACAGGTGACCATGTAGTGTATATGCTGAAAAATCATGTTGAAATAGTTGAAGAAGCT 1038
QY 1150 GGGAGACTGTTGGGTCAACCCCTGGATTTGCTTTTCAATTCACACGGATTAAGAAGAC 1209
DB 1039 GGAATAATTCCTTGGCCACTCTTTAGATTTAGTATTTTCCATACATCTGCAAGGAAGAT 1098
QY 1210 GGGTCAACCCGAGGAGCTCATTTACACCTCTCTTCCAGGCTCTTGCACCTTACGATCT 1269
DB 1099 GGCTCCCATTTGGAAGCGCAGTGGCCCTCTCTTCCCTGGTCCATGACACTTGGGACT 1158
QY 1270 GGCCTAGCAGCTATGCTGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATTGCTCTG 1329
DB 1159 GGTGTTGGCAAGATACGACAGACCTTTTGAACCTCTCTCGAAAGGCTCTGCTTAGTTGCTTG 1218

Qy	1330	TCGCTCATGCTGCTACCCAGTGAAGCAGAGAGATTGCGCTTTTGTCTCATCACCTCTG	1389
Db	1219	CGGCTTATGCCCTGAACCAAGTGAAGCCGAGAACTTAAGCACCTGACATCACCTGAT	1278
Qy	1390	GGAAAGATGAGTATTCAAATGGGTAGTTGGAGTCAGAGGAGTCTTTTGGAGATCATG	1449
Db	1279	GGAAAGATGAGTACTCACATGGATTGTTGCAAGTCAGAGAAGTCTTTTAGAGGTGATG	1338
Qy	1450	GCCGAGTTTCATCAGCAAAACCCCTCTTGGTGTGTTCTTGTGTCGAGTAGCCCTCGC	1509
Db	1339	GCTGCTTTTCCATCTGCAAAACCCCACTAGGTGTATTTTTGTGCAATAGTCTCTCGT	1398
Qy	1510	TTACCGCTCGATACTATTCTATCTCATCTCTCTCAAGTTTGTCTCCCTCAAGAATTCAT	1569
Db	1399	CTACAACCTGTTACTACTCCATCTCATCTCTCGCAAGATTGGGCCCAAGTAGAGTTTAT	1458
Qy	1570	GTGACGTGTCTTTTGTATATGTTCAAAGCCCTACCGAAGGGTTCACCCGAGGAGTGTGT	1629
Db	1459	GTTACATCCGACTAGTATATGTTGCCAACTCTTACTTGGTAGAATCCACAAGGGTGTGT	1518
Qy	1630	TCGACATGGATGAAGCATGAGTTCCTCAGGA-----TAGCTGGGCTCCT	1674
Db	1519	TCTACGTGGATGAAGATTCAGTTCTCGCGAGAAAAGTCAATGATCTAGTGGAGCCCCA	1578
Qy	1675	ATTTTCTTCCGAACGTCAAACTTCAAGTTACCGAGCTGACCCCTCAACTCCAATTATCATG	1734
Db	1579	ATCTTTATTCGAGCATCTAATTTCAAGTTACCATCCAACTTCAACTCCAATCGTTATG	1638
Qy	1735	GTGGGACCTGGTACAGGGTTAGCTCTCTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTC	1794
Db	1639	GTGGGACCTGGGACTGGGCTGGCACCTTTTAGAGGTTTCTGCAGGAAAGGATGGCACTA	1698
Qy	1795	AAGAAAATGGTGTCTCACTTGGCCGACAGTGTCTTTTTCGGATGTAGGAATCGTAAT	1854
Db	1699	AAAGAAGATGAGAAGAACTAGGTTTCTCTTCTCTTCTTCTGGGTGTAGAAATCGACAG	1758
Qy	1855	ATGACTTTCATTTATGAAGACGAACATAACAACTTCTGTGAAACGAGGAGTCATTTCGGAG	1914
Db	1759	ATGGACTTTATATACGAGGATGAGCTCAATAAATTTTGTGATCAAGCCGTAATATCTGAG	1818
Qy	1915	CTAGTTATTGCTCTTTTCACTGAAGGGGAAAAGAAGAAATATGTTCAACATAAGATGATG	1974
Db	1819	CTCATCATGCAATTTCTCCCTGAAGGAGCTCAGAGGAGTATGTTCAACATAAGATGATG	1878
Qy	1975	GAGAAAGCAACGATGATGATGATGATATCAGGGGACGGTATCTCTATGTGTGTGT	2034
Db	1879	GAGAAGGCAACACAAGTTTGGGATCTAATAAAGGAAAGAGGATATCTCTATGTATCGGT	1938
Qy	2035	GATGCCAAGGGAATGGCCAGAGATGTCATCGCACGTTGCATACCATTCGCCAAGAACAG	2094
Db	1939	GATGCTAAGGGCATGGCGGGAGCGTCCACCGAACTCTACACACCATTTGTTCAAGGACAG	1998
Qy	2095	GGACCCATGGAATCATCTGTCGCGAAGCTGCAAGTAAAGAACTCCAAGTTGAAGAACGA	2154
Db	1999	GAAGGTGTGATTCGTCAGAGGCAGAGGCTATAGTTAAGAACTTCAACCCGAAAGGA	2058
Qy	2155	TATCTAAGAGATGCTGGTGA	2175
Db	2059	TACCTCAGAGATGCTGGTGA	2079

RESULT 12

ATATR1G	2199 bp	mRNA	linear	PLN 01-JUN-1992
LOCUS	A.thaliana ATR1	mRNA for NADPH-cytochrome P450 reductase.		
DEFINITION	X66016			
ACCESSION	X66016			
VERSION	X66016.1	GI:16186		
KEYWORDS	ATR1 gene; NADPH-ferrihemoprotein reductase.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.			

REFERENCE	1 (bases 1 to 2199)	Mignote-Vieux,C., Kazmaier,M., Lacroute,F. and Pompon,D.M.
AUTHORS	Unpublished	
JOURNAL	2 (bases 1 to 2199)	Pompon,D.M.
REFERENCE	2 (bases 1 to 2199)	Direct Submission
AUTHORS	Pompon,D.M.	
TITLE	Submitted (11-MAY-1992)	D.M. Pompon, Centre de Genetique Mol du
JOURNAL	CNRS, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE	
FEATURES	Location/Qualifiers	
source	1..2199	
	/organism="Arabidopsis thaliana"	
	/mol_type="mRNA"	
	/strain="Heynh"	
	/sub_strain="Landsberg erecta"	
	/db_xref="taxon:3702"	
	/tissue_type="whole seedling"	
	/dev_stage="seedling (2 leaves)"	
gene	1..2199	
	/gene="ATR1"	
CDS	70..2148	
	/gene="ATR1"	
	/note="NADPH-cytochrome P450 reductase"	
	/codon_start=1	
	/product="NADPH-ferrihemoprotein reductase"	
	/protein_id="CAA46814.1"	
	/db_xref="GI:16187"	
	/db_xref="GOA:Q39035"	
	/db_xref="UniProt/TREMBL:Q39035"	
	/translation="MTSALYASDLFKQLKSI MGTSLSDDVVLVIATTSALVAGVFW LLEKTTADRSGELKPLMIPKSLMAKDEDDLDLGSKTRVSI FFGTGTAGGFAKA LSEELIKARYEKAARKVILDDYAADDDQYEEKLKKETLAFVCAVYDGEPTDNAARF SKWTFENERDIKLOOLAYGVFALGNQRYEHFNKIGI VLDESLCKKARKLIEVLGDS DDQSLDEDFNWAKSLWELDKLDEDDKSVATYTAIVIPEYRVVTHDPRTTQKSM ESNVANGNTTIDIHPCRVDAVQKELHEDHSDRSCIHLEFDISRTGITETGDDHVG YAENHEIVEEAKLLHSLDLVFSIHADKEDGSPLESAVPPFPFGPCTLGTGLARYA DLNLPKRSALVALAAYATPESEAKLHLTSPDKGDEYSQWIVASQRLLEWMAAFP SAKPLGVFFAAIAPLQPRYYSISSCODWAPSRVHTSALVYPTGRIHKGVCS WMKNVAPAEKSHCEKSGAIFIRASNFKLPSPSTPIVMVPGTGLAPRGFLQERMA KEDGELSGSLLFFCGRNQMDFIYEDELNNFDQGVISELIMAFSRGAQKEYVQHK NMEKAAQVMDLIKKEGYLYVCGDAKGMARDVHRTLHTTVQEQEGVSSSEAEAIKKLQ TEGRYLRDWN"	
ORIGIN		
Query Match	37.3%;	Score 987.6; DB 8; Length 2199;
Best Local Similarity	71.1%;	Pred. No. 1.3e-221;
Matches 1343; Conservative	0; Mismatches 529; Indels 18; Gaps 2;	
QY	310	ATAATTGATAAAGAAGAGGAGATTGAAGTTGATCTCGGTAAATAATTAAAGCTCACTATA 369
Db	271	ATGGCTAAGGACGAGATGATGATTTGGATTGGGATCCGGGAAGCTAGAGTCTCTATC 330
QY	370	TTTTTTGGTACTCAGACTGGTACTGCTGAAGATTGCTTAAGGCATTGGCAGAAAGAAATT 429
Db	331	TTCTTCGGTACCGACTGGAACAGCTGAGGATTGCTAAGGCATTATCCGAGAAATC 390
QY	430	AAGGCAAAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTCGATGACATATCGACCGCAG 489
Db	391	AAAGCGAGATATGAATAAAGACGACGTCAAAGTCATTGACTTGGATGACTATCTGCGCAT 450
QY	490	GATGATCAATATGAAGAGAAATTAAGAAGAAAGAGTCTTTGGTGTGTTTTTCATGTGAGCCACT 549
Db	451	GATGACCATGATGAAGAGAAATTAAGAAGAAACTTTGGGCATTTTTCTGTGTGCTACT 510
QY	550	TATGTGTATGGTGAGCCAACTGACAACTGTCGAGATTTTACAATGGTTCTACTCAGGAA 609
Db	511	TATGGAGATGGAGAGCGCTACTGACAATGCTGCCAGATTTTCAAAATGGTTTACGGAGGAA 570
QY	610	CATGAAGCGGAGAGTGGCTTCAGCAACTAATGTTGTTGTTTGGTTTGGTACCGTACCGT 669
Db	571	AATGAACGGGATATAAAGCTTCAACAACTAGCATATGGTGTGTTTGTCTCTGTAATCCG 630
QY	670	CAATACGAGCATTTTCAACAAGATCCGGGTAGATGTGGATGAGCAACTCGGTAAACAAGGT 729

631 CAATATGAACATTTTAAAGATCGGATAGTTCTTGATGAAGAGTTATGTAAGAAAGGT 690
QY
730 GCAAGGCGATTTGTTCAAGTGGGCTCGGTGACGATGATCAATGCAATGGAAGATGATTTT 789
Db
691 GCAAGGCGTCTTATTTGAAGTCGGTCTAGGAGATGATGATCAGAGCATTTGAGGATGATTTT 750
QY
790 ACTGCTTTGGGAGAAATTTGTTGGAGCTGAATTTGGATCAGTTGCTCAAAGATGAGGATGCT 849
Db
751 AATGCTTGGAAAGAAATCACTATGCTGAGTAGACAAGCTCTCAAAGACGAGGATGAT 810
QY
850 GCTCCTTCAGTGGCTACACGATATTTGCTACTGTTCTGAAATACAGGGTAGTGATCAC 909
Db
811 AAAAGT---GTGGCAACTCTTATACAGCTGTTATTCCTGAAATACCGGGTGGTCACTCAT 867
QY
910 GAAATACAGTTCGGGCTCTGGAGTATAAACAATAACTACTGTAACGGCGATGTTGCA 969
Db
868 GATCCTCGGTTTCACTCAAAATCAATGGAATCAATGTGGCAATGGAATATCACT 927
QY
970 TTTGATATTTCCATCCTTGCAGAACCAATTTGTTGCTCAACAAAGAGAGCTCCACAAACCC 1029
Db
928 ATTGACATTCATCATCCTCGAGATTTGATGTTGCTGTCAGAGGAGCTTCAACACAT 987
QY
1030 AGTCTGATAGATCTGATATACATCTGGAGTTGCAATATCAGGCTCTTCCCTTACATAT 1089
Db
988 GAATCTGATCGGCTCTTGCAATTCATCTGAGTTGACATATCCAGGACGGGTATTACATAT 1047
QY
1090 GAGACTGAGATCATGTTGGTGTATGCTGAGAACTGCGATGAACTGTCGAGGAGCA 1149
Db
1048 GAAACAGGTGACCATGAGTGTATATGCTGGAATCATGTTGAGATGTTGAAGAAGCT 1107
QY
1150 GGAAGAGTGTGGGTCAACCCCTGGATTTGCTGTTTCAATTCACACGGATAAAGAGAC 1209
Db
1108 GGAATATTTGCTGGCACTCTTTAGATTTAGTATTTCCATACATGCTGACAGAGAT 1167
QY
1210 GGGTACCCCGAGGAGCTCATTAACACCTCTTTCACAGGTCCTTTCACCTTACGATCT 1269
Db
1168 GGCTCCCAATGGAAGCGCAGTGGCGCTCTTTCCTGCTCATGACACTTGGACT 1227
QY
1270 GCCTAGCAGCTATGCTGATCTTTGAATCTCTAGAAAGCTTCTGATGCTCTG 1329
Db
1228 GGTGTCAGATACGACAGACCTTTTGAACCCCTCTCGAAAGTCTGCTGTTAGTTCCTG 1287
QY
1330 TCCGCTCATGATCTGTACCCAGTGAAGCAGAGATTTGGCTTTTGTTCATCACCTCTG 1389
Db
1288 GCGGCTATGCCACTGAACCAAGTGAAGCCGAGAACTTGAACACCTGACATCACCTGAT 1347
QY
1390 GGAAGATGAGTATCAAAATGGGTAGTTGGAAGTCAGAGGAGTCTTTTGGAGATCATG 1449
Db
1348 GGAAGAGTGAAGTACTCAATGATTTGTTGCAAGTCAGAGAGTCTTTTAGAGGTGATG 1407
QY
1450 GCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTCTGCTGAGTACCCCTGCG 1509
Db
1408 GCTGCTTTTTCATCTGCAAAACCCCACTAGGTGTATTTTGTCTGCAATAGTCTCTCGT 1467
QY
1510 TTACCGCTCGATATTTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAATTCAT 1569
Db
1468 CTACAACCTGTTACTACTCATCTCATCTGCGCAAGATTTGGGCGCAAGTAGATTCTAT 1527
QY
1570 GTGAGCTGCTTTAGTATATGCTAAAGCCCTTACCGGAAGGGTTTACCGAGGAGTGTGT 1629
Db
1528 GTTACATCGCACTAGTATATGTTGCTCAACTCTCTACTGTTAGATATCACAAGGGTGTGT 1587
QY
1630 TCCACATGATGATGAGTACGATTCCTCTCAGGA-----TAGCTGGGCTCTCT 1674
Db
1588 TCTACGTGGAATGAAGATGAGTCTCTGCGGAGAAAGTCAATGATGATGAGGAGCCCA 1647
QY
1675 ATTTTGTTCGAACTGCAAACTTCAAGTTACAGAGTACCCCTCAACTTCAATTTATCATG 1734
Db
1648 ATCTTTATTCGACATCTAATTTCAAGTTACCATCCAAACCTTCACTCAATCGTTATG 1707
QY
1735 GTGGGACCTGGTACAGGGTTAGCTCTCTTTTACAGAGGATTTCTGAGGAAAGATGGCCCTC 1794
Db
1708 GTGGGACCTGGGCTGGCACTTTTAGAGGTTTCTGAGGAAAGGATGGCACTA 1767

QY 1795 AAGGAAATGGTGTCTCAACTTGGCCAGCAGTGTCTCTTTTTCGATGTAGGAATCGTAAT 1854
Db 1768 AAGAAGATGGGAGAACTAGGTTTCATCTTTGCTCTTTTGGGTGTAGAAATCGACAG 1827
QY 1855 ATGGACTTCATTTATGAAGACCACTTCTGCGAAGAGGAGTCAATTTTCGGAG 1914
Db 1828 ATGGACTTTATATACGAGGATGAGTCAATAATTTTGTGATCAAGCGTAATATCTGAG 1887
QY 1915 CTAGTTATTTGCTTTTACGTGAAGGGGAAAGAAAGATATGTTTCAACATAAGATGATG 1974
Db 1888 CTATCATGGCATTTCTCCGTGAAGGAGCTCAGAAGGAGTATGTTTCAACATAAGATGATG 1947
QY 1975 GAGAAAGCAACGATGCTATGGAATGATATCAGGGGACGGTTATCTCTATGTTGTGGT 2034
Db 1948 GAGAGCGACGACAGTTTGGGATCTAATAAGGAAGAAGGATATCTCTATGTTATCGGT 2007
QY 2035 GATGCCAAGGGAATGSCCAGAGATGTCATCGACGTTGTCATACCACTTGCACGAAGACAG 2094
Db 2008 GATGCTAAGGCGATGCGAGGAGCGTCCACCGAACTCTACACACCATTTGTTACAGGAGCAG 2067
QY 2095 GGACCCATGGAATCATCTGCTGCCGAGCTGCAGTAAAGAACTCCAAGTTGAAGACGA 2154
Db 2068 GAAGGTGTCAGTTCTGTCAGAGGCGAGGCTATAGTTAAGAACTTCAAAACCGAAGAGA 2127
QY 2155 TATCTAAGAGATGCTCTGTTGATCGAATGTA 2184
Db 2128 TACCTCAGAGATGCTGTTGATGATGATA 2157

RESULT 13

A75959 LOCUS A75959 2114 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 1 from Patent WO9321326.
ACCESSION A75959
VERSION A75959.1 GI:6088149
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 2114)
Kazmaier, M. and Lacroute, F.
METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
Patent: WO 9321326-A 1 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)
FEATURES
Location/Qualifiers
1..2114
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/strain="LANSBERG ERECTA"
/db_xref="taxon:3702"
/dev_stage="FEUILLES"
/dev_stage="JEUNE PLANTULE STADE DEUX"
1..35
36..2114
/gene="ARA B"
36..2114
/gene="ARA B"
/codon_start=1
/product="NADPH CYTOCHROME P450 REDUCTASE"
/protein_id="CAB58575.1"
/db_xref="GI:6088150"

5'UTR

gene

CDS

SAXPPLGVFAAIAAPLPRYYSISSQDWPASRVHVTSALVYGPPTGRIHKGVCS
WMKNVPAEKSHCSGAPIFIRASNFKLPSNPSTPIVMVPGPTGLAPFRFLQERNAL
KEDGBELGSLLEFFGRNRQMDPIYDELNNFVDQVI SELINAFSREGAQKEYVQHK
MMEKAQVWDLIKEEGLYVCGDAKWARDVHRTLTHIVQOEGBVSSEAEAIKKLQ
TEGRYLRDVN"
2111..2114
/gene="ARA B"

3'UTR

ORIGIN

Query Match		37.2%	Score 985;	DB 6;	Length 2114;
Best Local Similarity		71.1%	Pred. No. 5.4e-221;		
Matches 1338;		Conservative 0;	Mismatches 525;	Indels 18;	Gaps 2;
Qy	310	ATAATTGATAAAGAAGAGGAGATTGAAGTTGATCCTCGTGAATAATTAAGCTCACTATA	369		
Db	237	ATGGCTAAGGACGAGGATGATGATTTGGATTTGGGATCCGGGAGACTAGAGTCTCTATC	296		
Qy	370	TTTTTTGGTACTCAGACTGCTACTGCTGAAGGATTTGCTAAAGCATTTGGCAGAGAAATT	429		
Db	297	TTCTTCGGTAGGACAGCTGGAACAGCTGAGGGATTTGCTAAGGCATTTATCCGAAGAAATC	356		
Qy	430	AAGGCAAAAGTACAAGAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGCGAGCCGAG	489		
Db	357	AAAGCGAGATATGAAAAGCAGCAGTCAAAGTCATTGACTTGGATGACTATGCTGCCGAT	416		
Qy	490	GATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTGGTGTGTTTTCATGTTAGCCACT	549		
Db	417	GATGACGAGTATGAAGAGAAATTTGAAGAAGGAAACTTTGGCATTTTCTGTGTGTACT	476		
Qy	550	TATGGTGATGGTGAGCCAACTGACAAATGCTGCCAGATTTTACAAATGGTTCACTCAGGAA	609		
Db	477	TATGGAGATGGAGGCCCTACTGACAACTGCTGCCAGATTTTCAAATGGTTTACGGAGAA	536		
Qy	610	CATGAAGGGGAGAGTGGCTTCAGCAACTAATCTATGGTGTGTTTGGTGTGGTAAACCGT	669		
Db	537	AATGAACGGGATATAAAGCTTCAACAACTAGCATATGGTGTGTTTGTCTCTGTAATCG	596		
Qy	670	CAATACGAGCATTTCAACAGATCGCGGTAGATGTGGATAGCAACTCGGTAAACAAGGT	729		
Db	597	CAATATATGAACATTTAATAAGATCGGGATAGTTCTTGAAGAAGTTATGTAAAGAAGGT	656		
Qy	730	GCAAAGCGCATGTTCAAGTGGGCTCGGTGACGATGATCAATGCTATTGAAGATGATTTT	789		
Db	657	GCAAAGCGCTCTTATGNAAGTGGTCTAGGAGATGATGATCAGAGCATTTGAGGATGATTTT	716		
Qy	790	ACTGCTTGGCGAGAAATGTTTGTGGA CTGAAATGGATCAGTTGCTCAAAGATGAGATGCT	849		
Db	717	AATGCTCTGGAAGAAATCACTATGGTCTGAGCTAGACAAAGCTCTCAAAGACGAGGATGAT	776		
Qy	850	GCTCCTTCAGTGGCTACACCGTATATGCTACTGTTCTCGTAATACAGGTTAGTATCAC	909		
Db	777	AAAAGT---GTGGCACTCTTATACAGCTGTTATTCCTGAAATACCGGGTGGTACTCAT	833		
Qy	910	GAAACTACGGTCCGGCTCTGGATGATAAACAATATACTCTCAACGCGCATGTTGCA	969		
Db	834	GATCCTCGGTTTGAACCTCAAAATCAATGGATCAAAATGTGCGCAATGGAATATCTACT	893		
Qy	970	TTTGATATTCCTCATCCTTCAGAACCAATTTGTTGCTCAACAAAGAGAGCTCCACAAACCC	1029		
Db	894	ATTGACATTCATCATCCCTGCAGAGTTGATGTTGCTGTG CAGAAGGAGCTTTCACACAT	953		
Qy	1030	AAGTCTGATAGATCCTGTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATAT	1089		
Db	954	GAAATCTGATCGGCTTGGCAATTCATCTCGAGTTTCGACATATCCAGGACGGGTATTTACATAT	1013		
Qy	1090	GAGACTGGAGATCATGTTGGTGTGTTATGCTGAGAACTGCGCATGAAACTGTCGAGGAGCA	1149		
Db	1014	GAAACAGGTGACCATGTAGTGTATATGCTGAAAATCATGTTGAGATAGTTGAAGAGCT	1073		
Qy	1150	GGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCAATTCACACGGATAAAGAAGAC	1209		
Db	1074	GGAAAAATTGCTGGCCACTCTTTAGATTTAGTATTTTCCATACATGCTGACAAAGGAAGAT	1133		

RESULT 14
ECU67186
LOCUS
DEFINITION

Eschecholtzia californica NADPH: ferrihemoprotein oxidoreductase
ECU67186 2561 bp mRNA linear PLN 06-MAR-1998

Qy	1210	GGGTCAACCCAGGAGCTCATTTACCACTCCTCTTCCAGGTCCTTGCACCTTACGATCT	126	
Db	1134	GGCTCCCATTTGGAAGCGCAGTGGCGCTCTCTTCCCTGGTCCAATGCACACTTGGGACT	1193	
Qy	1270	GCCTTAGCACGCTATGCTGATCTTTTGAATCTCTTAGAAGGCTTCTCTGATTGCTCTG	1329	
Db	1194	GGTTTGGCAAGATACGACAGACCTTTTGAACCTCTCTGAAAGTCTGCGTTAGTTGCTTG	1253	
Qy	1330	TCGCTTCATGCTATCTGTACCCAGTGAAGCAGAGAGATTGGCTTTTGTGTCATCACCTCTG	1389	
Db	1254	GCGGCTTATGCCACTGAACCAAGTGAAGCCGAGAACTTTAAGCACCTGACATCACCTGAT	1313	
Qy	1390	GGAAAGATGAGTATTTCAAAATGGGTAGTTTGAAGTCAGAGGAGTCTTTTGGAGATCATG	1449	
Db	1314	GGAAAGGATGAGTACTACAATGGAATGTTTGAAGTCAGAGAAGTCTTTTAGAGGTGATG	1373	
Qy	1450	GCGAGTTTCCATCAGAAAAACCCCTCTTGGTGTGTTCTTTGCTGCAGTAGGCCCTCGC	1509	
Db	1374	GCTGCTTTTCCATCTGCAAAACCCCACTAGGTGTATTTTTCGTGCAATAGCTCTCTCGT	1433	
Qy	1510	TTACCGCTCGATACTATTCTATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1569	
Db	1434	CTACAACCTCGTTACTTCTCATCTCATCTGCTCAAGATTGGCGGCCAAGTAGAGTTTCT	1493	
Qy	1570	GTGACGTGTCTTTAGTATATGTTCAAGCCCTACCGGAAGGTTTACCAGAGAGTGTGT	1629	
Db	1494	GTTTACATTCGCACTAGTATATGTTTCAACTCTCTACTGGTAGAATCCACAAGGGTGTGT	1553	
Qy	1630	TCGACATGGATGAAGCATGCAGTTCCTCAGGA-----TAGCTGGGCTCTCT	1674	
Db	1554	TCTACGTGGATGAAGAATGCAGTTCCTGCGAGAAAAGTCATGAATGTAGTGGAGCCCCA	1613	
Qy	1675	ATTTTGTTCGAACGTCACAACTTCAAGTTTACAGCTGACCCCTCAACTCAAATTCATG	1734	
Db	1614	ATCTTTATTCGAGCATCTAATTTCAAGTTACCATCCAACTTCAACTCCAAATCGTTATG	1673	
Qy	1735	GTGGGACCTGTTACAGGTTAGTCTCTCTTTCAGAGGATTTCTGCAGGAAAAGATGGCCCTC	1794	
Db	1674	GTGGGACCTGGGACTGGGCTGGCACCTTTTAGAGGTTTCTGCAGGAAAAGTAGGCACTA	1733	
Qy	1795	AAGGAAATGGTGTCTCAACTTGGCCAGCAGTGTCTTTTTCGGATGTAGGAATCGTAAAT	1854	
Db	1734	AAAGAAGATGGAGAAGAACTAGGTTTCATCTTTGCTCTCTTTGGGTGTAGAAAATCGACAG	1793	
Qy	1855	ATGGAATTCATTTATGAAGACGAACTAAACAACCTTCGTGGAAAGGAGGTCAATTCGGAG	1914	
Db	1794	ATGGAATTTATATACGAGGATGAGTCAATAATTTTGTGATCAAGGCGTAAATATCTGAG	1853	
Qy	1915	CTAGTTATTTGCTTTTTCAGTGAAGGGGAAAAGAGGAATATGTTTCAACATAGATGATG	1974	
Db	1854	CTCATCATGGCATTTCTCCGTGAAGGAGCTCAGAAGGAGTATGTTTCAACATAAGATGATG	1913	
Qy	1975	GAGAAAGCAACGGATGTATGGAATGTGATATCAGGGGACGGTTTATCTTATGTGTGTGT	2034	
Db	1914	GAGAGGACGACACAGTTTGGGATCTAATAAGGAGAGGATATCTCTATGTATGCGGT	1973	
Qy	2035	GATGCCAAGGGAATGGCCAGAGATGTCCAATCGCACTTCGATACCAATGCCCCAAGAACAG	2094	
Db	1974	GATGCTAAAGGGCATGGCGAGGACGTCACCCGAACTCTACACACCAATGTTGTCAGGAGCAG	2033	
Qy	2095	GGACCATGGAATCATCTGCTGCGGAAGCTGCAGTAAAGAAATCTCCAAGTTGAAGAACGA	2154	
Db	2034	GAAAGTGTGNTTCTGTCAGAGGACGAGGCTATAGTTAAGAAATCTTCAAACCGAAGGAGA	2093	
Qy	2155	TATCTAAGAGATGTCTGGTGA	2175	
Db	2094	TACCTCAGAGATGTCTGGTGA	2114	


```
mRNA, complete cds.
U67186
U67186.1 GI:2580498
Eschscholzia californica (California poppy)
Eschscholzia californica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Eschscholziaceae; Eschscholzia.
1 (bases 1 to 2561)
Rosco, A., Pauli, H.H., Priesner, W. and Kutchan, T.M.
Cloning and heterologous expression of NADPH-cytochrome P450
reductases from the Papaveraceae
Arch. Biochem. Biophys. 348 (2), 369-377 (1997)
98096363
MEDLINE
9434750
PUBMED
2 (bases 1 to 2561)
Pauli, H.H. and Kutchan, T.M.
Direct Submission
Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,
Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany
Location/Qualifiers
1..2561
/organism="Eschscholzia californica"
/mol_type="mRNA"
/db_xref="taxon:3467"
/notes="elicited cell suspension culture"
127..2244
/EC_number="1.6.2.4"
/functions="catalyzes the reduction of the
heme-thiolate-dependent monooxygenases and oxidases;
reduces cytochrome c"
/notes="cytochrome P-450 reductase"
/codon_start=1
/product="NADPH:ferrihemoprotein oxidoreductase"
/protein_id="AAC05022.1"
/db_xref="GI:2580498"
/translat="MEQTAVKVSLFDLFFSSILNGKLDPSNFSDDSSAAIILNREITLM
ILTTATAVFGCGFLVYMRSSNKKIVETQKLIKEPEPEVDGKKVFIFFGTQ
TGAEGFAPKALAEAKARYEKALFKVIDLDYDGDDEFEKLEKKEITLALFFIATYGD
GEPTDNAGRYQFTEGEBRMWMLQNGFVGLGNQVHEFNKVAKEVDEILTEQGG
KRIVPGLGDDQICEDDTAMRELVMPELDQLLDESCKTSVSTPYTAIVPEYRVF
HDATDASLDQKSNANGYTVYDVQPCRVANVVKELHTPVSDRSCIHLEFDISGTG
LTVETGHDGVGSENCVEVEERLLGYSDTVFSIHVDKEDGSPISGSALAPRPT
PCTLRALTAYDLINSPKKAALHALAAVASDPKEARLRLASPAKDEYAGWIIVAS
QRSLVMAEFPSKAPIGVFFAFAVAPRLLPRIYSSNNRMVPSRIHVTCALVHEKT
PAGRVHGVGCTWMSKSVLEENHDCSSWAPIFVRSQNFKLPAISVPIIMIGVGTGL
APFRFQMORLALKNSGVELGPAIFPGCRNQMDYIYEEELNPFVKEGAISVVVAF
SRGATKEYVQHKMAEKASYIWEIMISQAYLYVCGDAKGMWARDVHRTLHTIADEQGLS
DNSKTESLVKNLQMDGRYLQVW"
Query Match 36.6%; Score 969.8; DB 8; Length 2561;
Best Local Similarity 68.6%; Pred. No. 2.1e-217;
Matches 1375; Conservative 0; Mismatches 607; Indels 21; Gaps 2;
QY 202 ATTTTCATTATGTCACAACTAGCTTCAATGCTGATGGATTGGTTTCTTCGATGT 261
DB 250 ATTTTAATGATCTTAACAACTGCTATTGCTGTTTTTATCGGTTGTTGCTTCTAGTT 309
QY 262 ATGAAATCTTCGCTCTCAATCAAAACCTATTGAAACTTATAAACCATAATTGATAAA 321
DB 310 TGAGAGAGATCTTCAATAAGTCAGTAAATTTGTTGAAACTCAGAAATTCATCGTTGAA 369
QY 322 GAAGAAGAGGAGATTGAAGTTGATCTCGTGGTAAATTAAGCTCACTATATTTTTTGGTACT 381
DB 370 AAGGAACCAAGCACTGAAGTTGATGATGGAAGAGAGAGGTACTATCTTCTTTGGTACT 429
QY 382 CAGACTGGTACTGCTGAAGATTGCTTAAGGCAATTGCGCAGAGAAATTAAGGCAAGTAC 441
DB 430 CAAACTGGTACAGCTGAAGATTTCGCAAGGCACTTGCTGAAGAAGCAAAAGCAAGATAT 489
QY 442 AAGNAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATCGACCCGAGGATGATCAATAT 501
490 GAAAAGGCAATCTTTAAAGTGATTGATTCGGATGATTACGGACAGATGATGATGAATTC 549
502 GAAGAGAAATTAAGAAAGAGTCTTTGGTGTCTTTTTCATGTCGCCATCTTATGTCGTGT 561
550 GAAGAGAAATTAAGAAAGGAACTATAGCTCTTTTCTTTTGGCTACCTATGAGAGATGGT 609
562 GAGCCAACTGACAAATGCTCGAGATTTTACAAATGGTTCACTCAGGAACAATGAAGAGGGA 621
610 GAACCTACAGATTAATGCTCAAGATTTTATAAATGGTTTCAAGAGGGTAAAGAGAGGAA 669
622 GAGTGGCTTCAGCAACTAACTTATGCTGTTTGGTGGTAAACCGTCAATACAGCAT 681
670 ATGTGGCTCCAGAACTCTTCAATTTGGTCTCTCGGTCTAGGCAATAGACAGTATGAGCAT 729
682 TTCAACAAGATCGCGGTAGATGGATGAGCAACTCGGTAAACAAGGTGCAAGAGCGAATT 741
730 TTCAATAAGGTGGCAAAAGGAGGTGAGAGATACCTCACTGAACAGGGTGGGAAGCGTATT 789
742 GTTCAAGTGGGGCTCGGTGACGATGATCAATGATTAAGATGATTTTACTGCTTGGCGA 801
790 GTTCCCGTGGTCTAGGAGATGATCAATGATAGATAGATGATTTTCACTGCTGGCGG 849
802 GAATGTTGTGGAAGTGAATTTGGATCAGTTGCTCTCAAGATGAGGATGCTGCTCTTCAGTG 861
850 GAGTGGTATGGCTGAAATTTGGATCAGTTGCTCTCTTGTGAAAGTGATAAACAATCTGTT 909
862 GCTACACCGTATATGCTACTGTTCTGAATACAGGGTAGTGATTACAGAACTACGGTC 921
910 TCTACTCTTACACTGCCATCGTACCAGAAATACAGGGTAGTATTCATGATGCTACTGAT 969
922 GCGGCTCTGGATGATAAACAATTAATCTGCTAACGGGATGTTGCAATTTGATATTTCTC 981
970 GCATCTACTACAGACAAAACCTGGAGCAATGCANATGGCTACACTGTTTACGAGCTTCAA 1029
982 CATCTTTCGACAAACCAATTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGATAGA 1041
1030 CACCCATGACAGAGCAATTCGTTGTTAAGAGAGAGCTTCACACTCCAGTATCTGATCGT 1089
1042 TCCTGTATATCTGAGTTTGCATATACAGGCTCTTCCCTTACATATGAGATGAGAT 1101
1090 TCTTGTATTTCATCTGGAATTTGCACTTTCTGGCACTGGGCTACGATATGAACAGGAGAC 1149
1102 CATGTTGTGTTTATCTCTGAGACTCGGATGAACTGTGAGGAAGCAGGAGAGCTGTTG 1161
1150 CATGTCGGTGTCTTCTGAGAAATTTGTTTGAAGTTGTGAGGAAGCAGAGAGCTATTG 1209
1162 GGTCAACCCCTCGATTGCTGTTTCAATTCACACGGATAAAGAACGCGGTCACCC --- 1218
1210 GGTACTCTACAGACACCGTTTTCATTCATTCATTCATTCATTCCTGGAAGAGCGCTCA 1269
1219 CAGGGAAGCTCATATACACCTCTTCCAGAGTCTTTCGACCTTACATGATCGCCCTAGCA 1278
1270 AGTGAAGCGCTCTAGCTCTCTCTTTTCCAACTCCCTGCACTTAAGAAACAGCACTAACA 1329
1279 CGCTATGCTGATCTTTTGAATCTCTAGNAGAGGCTCTCTGATGCTCTGCTCGGCTCAT 1338
1330 CGATACGCTGATCTGTTTGAATCTCTCAAGAGGCTGCTCTGCAATGCTTTGGCTGCTTAT 1389
1339 GCATCTGTATCCCAAGTGAAGCAGAGATTTGCGCTTTTGTTCATCAGCTCTCTGGGAAAGAT 1398
1390 GCATCCGATCCAAAGAGAGCGAGCGACTAAGGTATCTTGGCTCTCTCTGCTGGAGGAC 1449
1399 GAGTATTTAAAATGGGTAGTTGGAACTCAGAGAGTCTTTTGGAGATCATGCGCGAGTTT 1458
1450 GAATACGCCAGTGGATAGTAGTAGTCAGAGAAAGTCTGCTAGTGTCTAGTGTGTAATTC 1509
1459 CCATCAGAAAACCCCTCTTGGTGTGTTTCTTGTGAGTAGTCCCTCGCTTACCGCT 1518
1510 CCATCAGAAAAGGCTCCAATTTGGGTTTTCTTTTGCAGCAGTAGTCTCTCGCTTGTGCGCA 1569
1519 CGATACCTATTTCTATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1578
```

Db 1570 AGATACTATTCTATTTCATCTTCCATAGGATGGTACCATTCTAGGATTTCATGTCCATGT 1629
Qy 1579 GCTTTAGTATATGGTCAAGCCCTACCGGAAGGTTTACCGAGAGTGTGTTCCGACATGG 1638
Db 1630 GCATTGGTGCATGAAAAACACCGCGAGTGGCGGTTTACAAAGAGTGTGTTTCAACCTGG 1689
Qy 1639 ATGAAGCATGCAGTTCTCTCAGGA-----TAGCTGGGCTCCTATTTTT 1680
Db 1690 ATGAAGAATTTCTGTCTTTTGGGAAGAAACCATGATGTCAGCAGCTGGGCACCAATCTTT 1749
Qy 1681 GTTCGAACGCTCAAACTTCAAGTTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGA 1740
Db 1750 GTCAGCAATCCAACTTCAAACTTCTGCTGATTTCTACAGTACCAATTATATGATGTT 1809
Qy 1741 CTTGGTACAGGTTAGTCTCTTTTCAAGAGATTTCTCGAGAAAGAAATGCCCTCAAGGAA 1800
Db 1810 CTTGGGACTGGATTAGTCTCTTTTAGGGGATTCATGCGAGGCGATTAGCTCTGAAGAAT 1869
Qy 1801 AATGGTGCTCAACTTGGCCCGCAGCTGCTCTTTTTCGGATGTAGGAATCGTATATGGAC 1860
Db 1870 TCTGGTGTAGAAATGGGACCCGCTATCTCTTTTGGATGCGAAGAACAGACAGATGGAT 1929
Qy 1861 TTCATTTATGAAGACGAATTAACAACCTTCGTGGAACGAGGAGTCAATTTTCGAGAGTAGTT 1920
Db 1930 TACATATGAAGAGGCTTAACAACCTTTGTGAAGAGGAGCTATCTCCGAAGTTGTT 1989
Qy 1921 ATTGCCTTTTACGTGAAGGGGAAAAGAAATATGTTTCAACATAGATGATGGAAGAA 1980
Db 1990 GTTGTCTTCTCAGTGCAGGAGCTACCAAGGAATAGCTCAACATAAATGGCGAGAG 2049
Qy 1981 GCAACGATGTATGGAATGATATCAGGGGAGGTTATCTCTATGTTGTTGTTGATGCC 2040
Db 2050 GCTTCTTACATCTGGGAAATGATCTCTCAAGGGTGCATTTTATGATGTGTTGATGCC 2109
Qy 2041 AAGGGAATGCCAGAGATGCCATCGCACCTTCATACCACTTCCCAAGAACAGGAGACC 2100
Db 2110 AAGGCATGCTAGAGAGCTACATCGAATCTCCACACCATTTGCCAGGACAGGATCT 2169
Qy 2101 ATGGAATCATCTGCTGCGAGCTGCAGTAAAGAACTCCAAAGTTGAAAGAACGATATCTA 2160
Db 2170 TTGGCAAACTCGAAGACCGAAAGCTTGGTGAAGAACTCAGATGATGGAAGGTATCTA 2229
Qy 2161 AGAGATGCTCTGGTGATCGAATGT 2183
Db 2230 CGTGATGTGGTGATGATTTT 2252

RESULT 15
AF302497
LOCUS AF302497
DEFINITION Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome P450 oxidoreductase isoform 2 mRNA, complete cds.
ACCESSION AF302497
VERSION AF302497.1 GI:13183563
KEYWORDS
SOURCE Populus balsamifera subsp. trichocarpa x Populus deltoides
ORGANISM Populus balsamifera subsp. trichocarpa x Populus deltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 2493)
Ro,D.K., Ehrling,J. and Douglas,C.J.
REFERENCE
AUTHORS Ro,D.K., Ehrling,J. and Douglas,C.J.
TITLE Cloning, Functional Expression, and Subcellular Localization of Multiple NADPH-Cytochrome P450 Reductases from Hybrid Poplar
JOURNAL Plant Physiol. 130 (4), 1837-1851 (2002)
PUBMED 12481067
REFERENCE
AUTHORS Ro,D.-K. and Douglas,C.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-2000) Botany, University of British Columbia, 6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
FEATURES
source 1. .2493

/organism="Populus balsamifera subsp. trichocarpa x Populus deltoides"
/mol_type="mRNA"
/db_xref="taxon:3695"
27..2165
/note="CPR2; enzyme"
/codon_start=1
/product="NADPH-cytochrome P450 oxidoreductase isoform 2"
/protein_id="AAK15260.1"
/db_xref="GI:13183564"
/translation="MQSSSSMKVSPLELMQAIKGVDPNTVSSSSGSAABMATLI
RENREVIILTTSIAVLGYVVLIWRSSGYQKVPVPPKPLIVKDLPEVEDDCKK
KTIIFGTQTGTAGFAKALAEAKARYEKAIFKTVLDLDYADDDDEYBEHKKESIA
IFPLATYGDEPTDNNARYKFTDGNERNGEWIKELPYAFVGLGNRQYKELIALIV
DXILNGGKQLVPVGLDDQMEDDFAAWRELLWPELDQLLLDDDDPTGVSTPYTA
AVAEYRVVLHDPEDAPLEDNNNSNANGHAIYDAQHPCRANVTVRRLHTPASDRSCTH
LEFDSGTGLVYGTGDHGYVCENLSEI VERALQLLGLSPDIYFTIHTNEODTPLSG
SALPPFPSSLTALTATRYADLLSSPKSALMALAAHATNPTEADRLHLASPGKDE
YAQWIVANHRSLLEVMAPPSAKPLGVFPASVAPRLLPYYSISSSPSMAPSRIHVT
CALVLEKTPAGRIHKGVCSWKNVAPLSEKSHDCSNAPIFVROSNFKLPADTKVPIIM
IGPGTGLAPFRGLQERLAQAGAEGLSSVILFFGCRNRQMDFIYEDELNNFVESGAL
SLSLVAFREGPTKEYVQHKMMQKASDIWNMI SQGGYLYVCGDAKGMKDVHRTLTI
VQEGSLDLSKTESFVKGLQMNRYLRDVM"

ORIGIN

Query Match 34.7%; Score 918.6; DB 8; Length 2493;
Best Local Similarity 68.8%; Pred. No. 2.4e-205;
Matches 1285; Conservative 0; Mismatches 569; Indels 15; Gaps 1;
Qy 323 AAGAAGAGCAGATTGAAGTTGATCTCGGTAAATAAAGCTCACTATATTTTGGTACTC 382
Db 298 AAGACCTCGAACTGAAGTTGATGATGGCAAGAAAGGTCCACATCTTTTCGGCACCC 357
Qy 383 AGACTGGTACTGCTGAAGGATTTGCTTAAGGCATTTGGCAGAAGAAATTAAGGCAAAAGTACA 442
Db 358 AAACCTGGTACTGCTGAAGGATTTGCTTAAGGCCTAGCTGAGGAGGCAAAAGCTCGGTATG 417
Qy 443 AGAAGCAGCTGTTAAAGTAGTTGACCTGGATGACTATGACCGCAGGAGTATGATCAATATG 502
Db 418 AGAAGCTATATTTAAACTGTTGATTTGGATGATTTATCGGAGGATGACGATGAATACG 477
Qy 503 AAGAGAAATTAAGAAAGAGTCTTTGGTGTCTTTTTCATGTTAGCCACTTATGTTGTTGGTG 562
Db 478 AAGAGAAATTAAGAAAGAGTCTTTGGCCATTTTCTTTGGCCCATATGAGATGGTG 537
Qy 563 AGCCAACTGCAATGCTGCGAGATTTTCAAAATGGTTCACTCAGGAACATGAAAGGGAG 622
Db 538 AGCCTACGATTAACGCCGCGAGGTTTATAAATGGTTTACAGATGGCAATGAGAGGGGG 597
Qy 623 AGTGGCTTCAGCAACTAATGTTGTTGTTTGGTTGGGTAAACCGTCAATAGGAGCAT 682
Db 598 AATGGCTTAAGAACTTCCATATGCTGTTTGGTCTTGGCAACAGGCAATACGAGCAT 657
Qy 683 TCAACAAGATCCGGTAGATGTGGATGAGCAACTCGGTAAACAAGGTGCAAAAGCGCAT 742
Db 658 TTAAATGAATTCCTATGTTGGATTAATAATCCTTGGCAACAGGTTGGAGAGCAGCTTG 717
Qy 743 TTCAAGTGGGGCTCGGTGACGATGATCAATGCAATGAAAGATGATTTTACTGTTGGCGAG 802
Db 718 TTCCAGTGGTCTTGGTGTATGATGATCAATGATGCAATGCAATGCAATGCGCATGCGAG 777
Qy 803 AATTGTTGGGATGAAATTTGGATCAGTTGCTCAAGATGAGGATGCTGCTCTCTCAGTGG 862
Db 778 AATTGTTGGGCTGAGTTGGACCAAGTTGCTTCTTGTATGGGATGATCAACCTGGTGT 837
Qy 863 CTACACCGTATATGCTACTGTTCTCTGAATACAGGTTAGTGTATTCACGAAACTACGGTCG 922
Db 838 CTACCCCTTATCTGCTGCGGAGAAATATCGGGTTGTATGATGATGATGATGATG 897
Qy 923 CGGCTCTGGATGATAAACAATAAATCTGCTTAACGGCGATGTTGCAATTTGATTTCTCC 982
Db 898 CACCATTAGAGGATGATACTGGAGTAATGCGAATGGTCTATGCTATTTATGATGCTCAGC 957

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:48 ; Search time 1301 Seconds
(without alignments)

12053.340 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002as:*

7: Geneseq2002bs:*

8: Geneseq2003as:*

9: Geneseq2003bs:*

10: Geneseq2003cs:*

11: Geneseq2003ds:*

12: Geneseq2004as:*

13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2645.8	99.9	2650	2 AAX08517	Aax08517 Poppy cyt
2	983.4	37.1	2114	2 AAQ51236	Aaq51236 Plant NAD
3	958.6	36.2	2558	2 AAX08520	Aax08520 Poppy cyt
4	895.4	33.8	2136	3 AAC44709	Aac44709 Arabidops
5	895.4	33.8	2136	6 ABZ12998	Abz12998 Arabidops
6	895.4	33.8	2136	8 ADA68489	Ada68489 Arabidops
7	875	33.0	2423	2 AAQ51237	Aaq51237 Plant NAD
8	859.8	32.5	2112	2 AAQ51238	Aaq51238 Plant NAD
9	849	32.0	2581	10 ADF89810	Adf89810 Triterpen
10	807.6	30.5	1863	6 AAD33078	Aad33078 Helianthu
11	807.6	30.5	1863	6 AAD26926	Aad26926 Helianthu
12	770.2	29.1	1985	12 ADJ10845	Adj10845 Recombina
13	586.4	22.1	2016	8 ADA70621	Ada70621 Rice gene
14	339.6	12.8	683	13 ADR60759	Adr60759 Cotton cd
15	272.2	10.3	609	13 ACN62895	Acn62895 Cotton ca
16	269.6	10.2	612	13 ACN62802	Acn62802 Cotton ca
17	263	9.9	555	13 ACN50810	Acn50810 Cotton an
18	257.4	9.7	638	13 ADR60436	Adr60436 Cotton cd
19	244.2	9.2	614	13 ACN51360	Acn51360 Cotton an
20	231.8	8.8	485	3 AAC35800	Aac35800 Zea may

ALIGNMENTS

RESULT 1

AAX08517
ID AAX08517 standard; DNA; 2650 BP.

XX
AC AAX08517;

XX
DT 19-JUL-1999 (first entry)

XX
DE Poppy cytochrome P450 reductase.

XX
KW Opium poppy; alkaloids; cytochrome P450 reductase; morphine; codeine;
KW oripavine; thebaine; transformation; crop yield; probe; primer; ss.

OS Papaver somniferum.

XX
FH Key Location/Qualifiers
CDS 124..2175

FT /*tag= a
FT /product= "Cytochrome P450 reductase"

XX
PN WO9911765-A1.

XX
PD 11-MAR-1999.

XX
PF 28-AUG-1998; 98WO-AU000705.

XX
PR 29-AUG-1997; 97AU-00008872.

XX
PA (JOHJ) JOHNSON & JOHNSON RES PTY LTD.

XX
PI Kutchan TM, Zenk MH, Atkins DG, Fiest AJ;

XX
XX WPI; 1999-214703/18.

DR P-PSDB; AAW85680, AAW85682.

XX
PT Nucleic acid encoding cytochrome P-450 reductase from poppy.

XX
PS Claim 3; Fig 9a; 58pp; English.

XX
CC Transforming plants with a nucleic acid molecule encoding cytochrome P450
CC reductase alters the yield and/or type of alkaloids produced. In opium
CC poppies it specifically increases the yield of medically useful alkaloids
CC such as morphine, codeine, oripavine and thebaine. Sequences

Abx61295 Arabidops
Adb58625 Toxicity-
Adb53276 Primary r
Abt42217 Toxicity
Abk63490 Rat seque
Adp72624 Renal tox
Abq85854 Arabidops
Aaq65716 Oxidoredu
Abk63444 Rat seque
Adb57857 Toxicity-
Adp72534 Renal tox
Aan81743 Plasmid p
Aan81746 Plasmid p
Aan81747 Plasmid p
Aan70925 Sequence
Aan81744 Plasmid p
Aan44409 Mouse mRN
Aan70605 Plasmid p
Abi99690 Mouse isc
Acf57504 Murine p4
Adj62862 Mouse p45
Abli5291 Drosophil
Aan81745 Plasmid p
Aaz93331 Partial s
Aaz93079 Partial s

21 207 7.8 416 10 ABX61295
22 195.6 7.4 2441 10 ADB58625
23 195.6 7.4 2441 10 ADB53276
24 195.6 7.4 2441 10 ABT42217
25 194 7.3 2401 6 ABK63490
26 194 7.3 2401 12 ADP72624
27 193.4 7.3 349 6 ABQ85854
28 192.8 7.3 1872 2 AAO65716
29 192.8 7.3 1872 6 ABK63444
30 192.8 7.3 1872 10 ADB57857
31 192.8 7.3 1872 12 ADP72534
32 192.8 7.3 3435 1 AAN81743
33 192.8 7.3 3435 1 AAN81746
34 191.4 7.2 3399 1 AAN81747
35 191.2 7.2 2037 1 AAN70925
36 191.2 7.2 3453 1 AAN81744
37 189.2 7.1 2461 11 ACN44409
38 187.6 7.1 2450 1 AAN70605
39 187.4 7.1 2457 6 ABI99690
40 187.4 7.1 2457 12 ACF57504
41 187.4 7.1 2457 12 ADJ62862
42 177.4 6.7 2721 4 ABLI5291
43 170.4 6.4 3489 1 AAN81745
44 169.4 6.4 3310 3 AAZ93331
45 169.4 6.4 3311 3 AAZ93079

complementary to the coding sequence of cytochrome P450 reductase are useful as probes, primers and antisense sequences, or for design of ribozymes. Transformation with DNA encoding the cytochrome P450 reductase allows regulation of the total alkaloid content and of the relative proportions of individual alkaloids produced. Increasing the alkaloid content of poppy straw should reduce the cost of alkaloid production. Cytochrome P450 reductase is the rate-limiting enzyme in biosynthesis of alkaloids in poppies. Peptide fragments of the cytochrome P450 reductase are described in AA085672-W85678

XX SQ Sequence 2650 BP; 766 A; 514 C; 606 G; 764 T; 0 U; 0 Other;

Query Match 99.9%; Score 2645.8; DB 2; Length 2650;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2647; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCACGAGCTCTTAGTATCTTCTAGGGTTTCAGAAAGACACGGAGAGCAAAAGT 60
DB 1 CGGCACGAGCTCTTAGTATCTTCTAGGGTTTCAGAAAGACACGGAGAGCAAAAGT 60

QY 61 CGAATCTACTGAAATACATTCGATTGCTTCTCTCTGTTTAAAGCTTCAGAGTCTGTGTA 120
DB 61 CGAATCTACTGAAATACATTCGATTGCTTCTCTCTGTTTAAAGCTTCAGAGTCTGTGTA 120

QY 121 ATTATCGGTTTCAATTAATTAGCTAATTCGATTGAATCGATGTAGGAATATCAATAGGA 180
DB 121 ATTATCGGTTTCAATTAATTAGCTAATTCGATTGAATCGATGTAGGAATATCAATAGGA 180

QY 181 TCAGAAATATATTTCTGACCCAAATTTTCATTATGCTCACAACCTGTAGCTTCAATGCTGATT 240
DB 181 TCAGAAATATATTTCTGACCCAAATTTTCATTATGCTCACAACCTGTAGCTTCAATGCTGATT 240

QY 241 GGATTTGGTTTCTCGCATGTATGAATCTTCTCTCTCAATCAAAAACCTATTGAAACT 300
DB 241 GGATTTGGTTTCTCGCATGTATGAATCTTCTCTCTCAATCAAAAACCTATTGAAACT 300

QY 301 TATAAACCAATTAATTGATAAAGAGAGGAGATTGAAGTTGATCCTGGTAAATTAAG 360
DB 301 TATAAACCAATTAATTGATAAAGAGAGGAGATTGAAGTTGATCCTGGTAAATTAAG 360

QY 361 CTCACATATATTTTGGTACTCAGACTGGTACTGCTGAAGGATTTGCTAAGGCATTGGCA 420
DB 361 CTCACATATATTTTGGTACTCAGACTGGTACTGCTGAAGGATTTGCTAAGGCATTGGCA 420

QY 421 GAAGAAATTAAGCAAAAGTACAAGAACGAGTTGTTAAAGTAGTTCACCTGGATGACTAT 480
DB 421 GAAGAAATTAAGCAAAAGTACAAGAACGAGTTGTTAAAGTAGTTCACCTGGATGACTAT 480

QY 481 GCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAGAGAGTCTTTGGTGTTCATG 540
DB 481 GCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAGAGAGTCTTTGGTGTTCATG 540

QY 541 GTAGCCACTTATGGTGATGTGAGCCAACTGACAACTGTCGAGATTTTACAAATGGTTC 600
DB 541 GTAGCCACTTATGGTGATGTGAGCCAACTGACAACTGTCGAGATTTTACAAATGGTTC 600

QY 601 ACTCAGGAACATGAAGGGGAGAGTGGCTTCAGCAACTAATCTATGGTGTTCGTTTG 660
DB 601 ACTCAGGAACATGAAGGGGAGAGTGGCTTCAGCAACTAATCTATGGTGTTCGTTTG 660

QY 661 GGTAAACCGTCAATACGAGCAATTTCAACAAGATCGCGTAGATGTGAATGAGCAACTCGGT 720
DB 661 GGTAAACCGTCAATACGAGCAATTTCAACAAGATCGCGTAGATGTGAATGAGCAACTCGGT 720

QY 721 AAAACAAGGTCAAAGCGCATTTGTTCAAGTGGGCTCGGTGACCATGATCAATGCATTGAA 780
DB 721 AAAACAAGGTCAAAGCGCATTTGTTCAAGTGGGCTCGGTGACCATGATCAATGCATTGAA 780

QY 781 GATGATTTTACTGCTTGGCGAGAAATTTGTTGTGACTGAATTTGGATCAGTTGCTCAAAGAT 840
DB 781 GATGATTTTACTGCTTGGCGAGAAATTTGTTGTGACTGAATTTGGATCAGTTGCTCAAAGAT 840

QY 841 GAGGATGCTCTCTTCAGTGGGTACACCGTATATTGCTACTGTTCTCTGATACAGGGTA 900

DB 841 GAGGATGCTCTCTTCAGTGGGTACACCGTATATTGCTACTGTTCTCTGAAATACAGGGTA 900

QY 901 GTGATTACAGAAACTACGGTCGCGGTCTGGATGATAAACACATAAATACTGCTAACGGC 960
DB 901 GTGATTACAGAAACTACGGTCGCGGTCTGGATGATAAACACATAAATACTGCTAACGGC 960

QY 961 GATGTTGCAATTTGATATTCTCCATCTTGCAGAAACCATTTGTTGCTCAACAAAGAGAGCTC 1020
DB 961 GATGTTGCAATTTGATATTCTCCATCTTGCAGAAACCATTTGTTGCTCAACAAAGAGAGCTC 1020

QY 1021 CACAAACCAAGTCTGATAGATCCTGTATACATCTGGAGTTCGACATATCAGGCTCTTCC 1080
DB 1021 CACAAACCAAGTCTGATAGATCCTGTATACATCTGGAGTTCGACATATCAGGCTCTTCC 1080

QY 1081 CTTACATATGAGACTGGAGATCATGTTGGTGTATGCTGAGAACTGCGATGAAAATGTGC 1140
DB 1081 CTTACATATGAGACTGGAGATCATGTTGGTGTATGCTGAGAACTGCGATGAAAATGTGC 1140

QY 1141 GAGGAAGCAGGAAAGCTGTTGGGTCAAACCCCTGGATTTGCTGTTTCAATTCACACGGAT 1200
DB 1141 GAGGAAGCAGGAAAGCTGTTGGGTCAAACCCCTGGATTTGCTGTTTCAATTCACACGGAT 1200

QY 1201 AAAGAGACGGCTCACCCAGGGAGCTCATTTACACCTCTTCCAGGTCTCTGCACC 1260
DB 1201 AAAGAGACGGGTCAACCAGGGAGCTCATTTACACCTCTTCCAGGTCTCTGCACC 1260

QY 1261 TTACGATCTGCCCTAGCAGCTATGCTGATCTTTTGAATCTCTAGAAAGGCTTCTCTG 1320
DB 1261 TTACGATCTGCCCTAGCAGCTATGCTGATCTTTTGAATCTCTAGAAAGGCTTCTCTG 1320

QY 1321 ATTGCTCTGCTCGCTCATGCTATCCAGTGAAGCAGAGAGATGCGCTTTTGTGTA 1380
DB 1321 ATTGCTCTGCTCGCTCATGCTATCCAGTGAAGCAGAGAGATGCGCTTTTGTGTA 1380

QY 1381 TCACCTCTGGGAAAGATGAGTATCAAAATGGTAGTTGGAGTTCAGAGGAGTCTTTTG 1440
DB 1381 TCACCTCTGGGAAAGATGAGTATCAAAATGGTAGTTGGAGTTCAGAGGAGTCTTTTG 1440

QY 1441 GAGATCATCGCCGAGTTCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGTCAGTA 1500
DB 1441 GAGATCATCGCCGAGTTCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGTCAGTA 1500

QY 1501 GCCCTCGCTTACCGGCTCGATATTTCTATCTATCTCTCTCTCTCTCTCTCTCTCTCT 1560
DB 1501 GCCCTCGCTTACCGGCTCGATATTTCTATCTATCTCTCTCTCTCTCTCTCTCTCTCT 1560

QY 1561 AGAATTCATGTCGAGTGTCTTTAGTATATGTCAAAGCCCTACCGGAAGGTTTCAACCGA 1620
DB 1561 AGAATTCATGTCGAGTGTCTTTAGTATATGTCAAAGCCCTACCGGAAGGTTTCAACCGA 1620

QY 1621 GGAGTGTGTTTCGACATGGAAGCATGCAGTTCCTCAGGATAGCTGGGCTCTATTTTT 1680
DB 1621 GGAGTGTGTTTCGACATGGAAGCATGCAGTTCCTCAGGATAGCTGGGCTCTATTTTT 1680

QY 1681 GTTCGAAACGTCAAACTTCAAAGTTACAGCTGACCCCTCAAATTCATATCATGTTGGGA 1740
DB 1681 GTTCGAAACGTCAAACTTCAAAGTTACAGCTGACCCCTCAAATTCATATCATGTTGGGA 1740

QY 1741 CCTGGTACAGGGTATAGTCTCTTTGAGGATTTCTGACGAAAGATGCGCTCAAGGAA 1800
DB 1741 CCTGGTACAGGGTATAGTCTCTTTGAGGATTTCTGACGAAAGATGCGCTCAAGGAA 1800

QY 1801 AATGTTGCTCAACTTGGCCACGAGTGTCTTTTTCGATGTAGGAATCGTAATATGGAC 1860
DB 1801 AATGTTGCTCAACTTGGCCACGAGTGTCTTTTTCGATGTAGGAATCGTAATATGGAC 1860

QY 1861 TTCAATTTATGAAGCAAACTTAAACAACTTCGTGGAAACGAGGAGTCAATTTCCGAGCTAGTT 1920
DB 1861 TTCAATTTATGAAGCAAACTTAAACAACTTCGTGGAAACGAGGAGTCAATTTCCGAGCTAGTT 1920

QY 1921 ATTGCTCTTTTCAGTGAAGGGGAAAGAGGAATATGTTTCAACATAGATGATGGAGAA 1980

```
Db 1921 ATTGCTCTTTTACGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGGAGAAA 1980
Qy 1981 GCAACGATGTATGGAATGTATATCAGGGGACGGTTATCTCTATGTGTGTGTATGCC 2040
Db 1981 GCAACGATGTATGGAATGTATATCAGGGGACGGTTATCTCTATGTGTGTGTATGCC 2040
Qy 2041 AAGGGAATGGCCAGAGATGTCATCGCACGTTGCCATACCATTTGCCCAAGAACAGGACCC 2100
Db 2041 AAGGGAATGGCCAGAGATGTCATCGCACGTTGCCATACCATTTGCCCAAGAACAGGACCC 2100
Qy 2101 ATGGAATCATCTGCTCGGAGCTGCAAGTAAGAACTCCAAAGTGAAGAACGATATCTA 2160
Db 2101 ATGGAATCATCTGCTCGGAGCTGCAAGTAAGAACTCCAAAGTGAAGAACGATATCTA 2160
Qy 2161 AGAGATGCTGCTGATCGAATGTAGCTTGCACGTTGCCAAGTCCCTTTCTTGGCTGCTGTTA 2220
Db 2161 AGAGATGCTGCTGATCGAATGTAGCTTGCACGTTGCCAAGTCCCTTTCTTGGCTGCTGTTA 2220
Qy 2221 TGGTTCTATTATATTATGATCCTCTCTGAAATCCCAAGCACITTCAGACATCCCTC 2280
Db 2221 TGGTTCTATTATATTATGATCCTCTCTGAAATCCCAAGCACITTCAGACATCCCTC 2280
Qy 2281 GATTCCTCTCCAGTGGTCCAAATCGAAGCTCGGTATTAATTCAGAGCAGTGAATGTG 2340
Db 2281 GATTCCTCTCCAGTGGTCCAAATCGAAGCTCGGTATTAATTCAGAGCAGTGAATGTG 2340
Qy 2341 ACTACATGAGAGCAACATCGAATACCATGATTAAGATTAAGATTAAGATTAAGATTA 2400
Db 2341 ACTACATGAGAGCAACATCGAATACCATGATTAAGATTAAGATTAAGATTAAGATTA 2400
Qy 2401 GAACAATGTTACAGGCAAACTGTGTTGCTTAATAATAATTTACACCATGGGTGGGA 2460
Db 2401 GAACAATGTTACAGGCAAACTGTGTTGCTTAATAATAATTTACACCATGGGTGGGA 2460
Qy 2461 CAACACTGAAACAGTATTAGCTATACCAACAAAGTTATGCAAGAAACACAAACTAGTTA 2520
Db 2461 CAACACTGAAACAGTATTAGCTATACCAACAAAGTTATGCAAGAAACACAAACTAGTTA 2520
Qy 2521 GATCTCTCTTGGATTGATTACTGTAAGTTCTAAACAGATGATAGATGATGATTAAGA 2580
Db 2521 GATCTCTCTTGGATTGATTACTGTAAGTTCTAAACAGATGATAGATGATGATTAAGA 2580
Qy 2581 TTCTTGTTTCTTATGCTACCGAGGAGTATATTAATGCAATTTAGAGTTTGGAGAAA 2640
Db 2581 TTCTTGTTTCTTATGCTACCGAGGAGTATATTAATGCAATTTAGAGTTTGGAGAAA 2640
Qy 2641 AAAAAAAAAA 2649
Db 2641 AAAAAAAAAA 2649

RESULT 2
ID AAQ51236 standard; cdna; 2114 BP.
XX
AC AAQ51236;
XX
DT 25-MAR-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE Plant NADPH cytochrome P450 reductase (ara B).
XX
KW NADPH cytochrome P450 reductase; functional complementation;
KW identification; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
XX CDS 36..2114
FT /*tag= a
FT /product= "NADPH cytochrome P450 reductase."
FT misc_difference 510..512
FT /*tag= c
FT
```

PA	(ORSA-) ORSAN.	
XX	Kazmaier M, Lacroute F, Mignotte-Vieux C, Minet M, Pompon D;	
PI	WPI; 1993-351736/44.	
XX	P-PSDB; AAR43581.	
DR	New DNA encoding plant NADPH cytochrome P450 reductase - cloned by	
PT	functional complementation in yeast, also recombinant enzyme useful in	
PT	P450 mediated bioconversion processes.	
XX	Claim 11; Fig 9; 79pp; French.	
XX	A new method for determining whether a DNA sequence encodes an NADPH	
CC	cytochrome P450 reductase involves transforming yeasts with plasmids of a	
CC	total cDNA bank of plant(s). The yeasts used in the procedure are	
CC	incapable of producing their own NADPH cytochrome P450 reductase. They	
CC	are then exposed to a cytochrome P450 inhibitor at a level which is	
CC	lethal to the yeast cells but not to cells which, because of the	
CC	transformation, now contain an active NADPH cytochrome P450 reductase.	
CC	Surviving clones are then isolated and plasmid DNA extracted. The gene is	
CC	inserted into the plasmid at a site which places it under the control of	
CC	an inducible promoter. (Updated on 25-MAR-2003 to correct PN field.)	
XX	Sequence 2114 BP; 603 A; 400 C; 542 G; 569 T; 0 U; 0 Other;	
SQ	Query Match 37.1%; Score 983.4; DB 2; Length 2114;	
	Best Local Similarity 71.1%; Pred. No. 1.5e-254;	
	Matches 1337; Conservative 0; Mismatches 526; Indels 18; Gaps 2;	
Qy	310 ATAATTGATAAAGAAGAGGAGATTGAAGTTGATCTCTGGTAAATAATTAACTCAGTATA	369
Db	237 ATGGCTAAGGACGAGGATGATGATTGGATTGGGATCCGGGAAGACTAGAGTCTCTATC	296
Qy	370 TTTTGTGGTACTCAGACTGGTACTGCTGAAGATTGCTTAAGGCATTGGCAGAGAATAAT	429
Db	297 TTCTTCGGTACGAGACTGGAACAGCTGAGGATTTGCTTAAGGCAATTATCCGAAGAATC	356
Qy	430 AAGCGAAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGCAGCCGAG	489
Db	357 AAGCGAGATATGAAAGACGACGATCAAAGTCATTGACTTTGGATGACTATGCTGCCGAT	416
Qy	490 GATGATCAATATGAAGAGAAATTAAGAAGAGAGTCTTTGGTGTTTTTCATGGTAGCCACT	549
Db	417 GATGACCAATATGAAGAGAAATTAAGAAGAGAACTTTGGGCATTTTCTGTGTGCTACT	476
Qy	550 TATGGTGTGGTGGAGCCAACTGACAACTGCTGGAGATTTTCAAAATGGTTCACTCAGGAA	609
Db	477 TATGGAGATGGAGAGCTTACTGACAACTGCTGCCAGATTTTCAAAATGGTTCACGGAGAA	536
Qy	610 CATGAAGGGGAGTGGCTTCAGCAACTAACTTATGGTGTTTTGGTTCGGGTAAACCGT	669
Db	537 AATGAACGGGATATAAAGCTTCAACATGACATATGGTGTGTTTGGTGTGTTAATCGC	596
Qy	670 CAATACGAGCATTTCAACAGATTCGGGTAGATGTTGGATGAGCAACTCGGTAAACAAGGT	729
Db	597 CAATATGAACATTTTAAAGATCGGATAGTCTTGTGATGAAGATTTATGTAAGAAGGT	656
Qy	730 GCAAGGCGATTGTTCAAGTGGGCTCGGTGACGATGATCAATGCAATGGAAGATGATTTT	789
Db	657 GCAAGCGCTTATTGAAGTCCGCTTAGGAGATGATGATCAGAGCAATTTGAGGATGATTTT	716
Qy	790 ACTGCTTGGCGAAATGTTGTGGACTGAATTTGGATGACTGCTCAAGATGAGGATGCT	849
Db	717 AATGCTTGGAAAGATCACTATAGGCTTGAGCTAGACAAAGCTCCTCAAGACGAGGATGAT	776
Qy	850 GCTCCTTCAGTGGCTACACCGTATATTGCTACTGTTTCTTGAATACAGGGTATGATTCAC	909
Db	777 AAAAGT---GTGGCAACTCTTATACAGCTGTTATTCTCGAATACCGGCTGCTGACTCAT	833
Qy	910 GAAACTACGGTTCGGCTCTGGATGATGATAAACAATATAATATCTGCTAAACGGCGATTTGCA	969
Db	834 GATCCTCGGTTTACAACCTCAAAAATCAATGGAATCAATGTTGGCCAAATGGAATACTACT	893
Qy	970 TTTTGATATTCTCCATCTCTTGCAAGAACCAATTTGCTCAACAAAGAGAGCTCCCAAAACCC	1029
Db	894 ATTGACATTTCAATCATCCCTCGAGAGTTGATGCTGTGCGAAGAGGAGCTTCCACACACAT	953
Qy	1030 AAGTCTGATAGATCTCTGTATATACATCTGGAGTTTCACATATACAGGCTCTTCCCTTACATAT	1089
Db	954 GAATCTGATCGGCTCTTGCAATTCATCTCGAGTTTCACATATCCAGAGCGGGTATTACATAT	1013
Qy	1090 GAGACTGGAGATCATGTTGGTGTATTATGCTCAGAACTCGCATGAAACTGTGAGGAAGCA	1149
Db	1014 GAAACAGGTGACCATGTAGGTGATATGCTGAAATCATGTTTGAGATAGTTGGAAGAAGCT	1073
Qy	1150 GGGAAAGCTGTGGGTCAACCCCTGGATTGCTGTTTCAATTCACCGGATATAAAGAGAC	1209
Db	1074 GGGAAATTTGCTTGGCCACTCTTTAGATTAGTATTTTCCATACATGCTGACAGGAAGAT	1133
Qy	1210 GGGTACCCCGAGGAAGCTCAATTACACCTCTCTTTCCAGAGTCTTTGGACCTTACGATCT	1269
Db	1134 GGGTCCCCATTGGAAGGCGAGTGGCGCTCTCTTTTCCCTGCTCATGACACATTTGGGACT	1193
Qy	1270 GGCCTAGCAGCTATGCTGATCTTTTGAATCCTCTGAAAGGCTCTCTGATTGCTGCTG	1329
Db	1194 GGTGTGGCAAGATACGCAGACCTTTTGAACCTCTCTGAAAGTCTGGCTTAGTTGGCTTG	1253
Qy	1330 TCCGCTCATGCTATCTGTATACCCAGTGAAGCAGAGAGATTGGCTCTTTTGTTCATCACCTCTG	1389
Db	1254 GGGGCTATGCCACTGAACCAAGCGAGCCGAGAACTTAAGCACCTGACATCACCTGAT	1313
Qy	1390 GGAAGAATGAGTATTTCAAAATGGGTAGTTGGAAGTACAGAGAGTCTTTTGGAGATCATG	1449
Db	1314 GGAAGGATGAGTACTCAATGGATTGTTCAAGTTCAGAGAGTCTTTTAGAGGTGATG	1373
Qy	1450 GCGAGTTTCCATCAGCAAAACCCCTCTGCTGTGTTCTTTGCTGAGTAGCCCTCGC	1509
Db	1374 GCTGCTTTTCCATCTGCAAAACCCCTACTAGGTGATTTTGTGCTCAATAGCTCTCTCGT	1433
Qy	1510 TTACCGCTTCGATATCTATTCTATCTCATCTCTCTCAAGTTTGCTCTCTCAAGAATTCAT	1569
Db	1434 CTACAACTCTGTTACTACTCTCATCTCTGCCAAGATTGGGCGCCAAAGTAGAGTTCAT	1493
Qy	1570 GTGAGTGTGCTTTTATGATATAGGTCAAAAGCCCTACCGGAAGGGTTTACCGAGAGAGTGTGT	1629
Db	1494 GTTACATCGCACTAGTATATAGTCCAACTCTACTGTTGTAAGTCCCAAGGGTGTGTGT	1553
Qy	1630 TCGACATGATGAACATGCACTGCTCTCAGGATCTCTCAGGATCTCTCAGGATCTCTCT	1674
Db	1554 TCTACGTGATGAAGATGCAAGTCTCTCGGAGAAAGTCAATGATGTAGTGGAGCCCA	1613
Qy	1675 ATTTTGTTCGAACTCAAACTTCAAGTTTACAGCTGACCCCTCAACTCCAAATTTATCATG	1734
Db	1614 ATCTTTATTCGAGCATCTAAATTTCAAGTTTACCACTCAACCTTCAACTCCATGCTTATG	1673
Qy	1735 GTGGGACCTGGTACAGGGTTAGTCTCTTTTCAGAGATTTTTCGAGGAAAGATGCGCCCT	1794
Db	1674 GTGGGACCTGGGACTGGGCTGGCACTTTTATAGAGGTTTCTTCGAGGAAAGGATGGCACTA	1733
Qy	1795 AAGGAAATGGTGTCTCAACTTGGCCCGACAGTGTCTTTTTCGATGTAGGAAATCGTAAT	1854
Db	1734 AAAGAAGATGGAAGAAAGAACTAGGTTTCTTTTGTCTCTTTTGGGTGTAGAAATTCGACAG	1793
Qy	1855	

Qy	2035	GATGCCAAGGAATGCCAGAGATGTCATCGACGTTGCAATACCATTCGCCAAGAAGACAG	2094
Db	1974	GATGCTAAGGGCATGGGAGGAGCGTCCACCGAACTCTTACACACCATTTGTTTCAGGAGCAG	2033
Qy	2095	GGACCCATGGAATCATCTGCTGCGGAAGCTGCAGTAAAGAACTCCCAAGTTGAGAGAACGA	2154
Db	2034	GAAGGTGTGAGTTGCTTACAGGCGAGAGGCTATAGTTAAGAACTTCAACCGAAGGAAGA	2093
Qy	2155	TATCTAAGAGATGTCCTGGTGA	2175
Db	2094	TACCTCAGAGATGTCGTGTA	2114
RESULT 3			
AA	AX08520	standard; DNA; 2558 BP.	
XX	XX	AX08520;	
AC	AC		
XX	XX	19-JUL-1999 (first entry)	
DT	DT		
XX	XX	Poppy cytochrome P450 reductase.	
DE	DE		
XX	XX	Opium poppy; alkaloids; cytochrome P450 reductase; morphine; codeine; oripavine; thebaine; transformation; crop yield; probe; primer; ss.	
KW	KW		
XX	OS	Eschscholzia californica.	
XX	XX		
PH	PH	Key	Location/Qualifiers
FT	FT	CDS	127..2241
FT	FT		/*tag= a
FT	FT		/product= "Cytochrome P450 reductase"
XX	XX	WO9911765-A1.	
XX	XX		
PD	PD	11-MAR-1999.	
XX	XX		
PF	PF	28-AUG-1998; 98WO-AU000705.	
XX	XX		
PR	PR	29-AUG-1997; 97AU-00008872.	
XX	XX		
PA	(JOHJ)	JOHNSON & JOHNSON RES PTY LTD.	
XX	XX	Kutchan TM, Zenk MH, Atkins DG, Fist AJ;	
PI	PI		
XX	XX	WPI; 1999-214703/18.	
DR	DR	P-PSDB; AAW85681, AAW85683.	
DR	DR		
XX	XX		
PT	PT	Nucleic acid encoding cytochrome P-450 reductase from poppy.	
XX	XX		
PS	PS	Claim 3; Fig 9b; 58pp; English.	
XX	XX		
CC	CC	Transforming plants with a nucleic acid molecule encoding cytochrome P450 reductase alters the yield and/or type of alkaloids produced. In opium poppies it specifically increases the yield of medically useful alkaloids such as morphine, codeine, oripavine and thebaine. Sequences complementary to the coding sequence of cytochrome P450 reductase are useful as probes, primers and antisense sequences, or for design of ribozymes. Transformation with DNA encoding the cytochrome P450 reductase allows regulation of the total alkaloid content and of the relative proportions of individual alkaloids produced. Increasing the alkaloid content of poppy straw should reduce the cost of alkaloid production. Cytochrome P450 reductase is the rate-limiting enzyme in biosynthesis of alkaloids in poppies. Peptide fragments of the cytochrome P450 reductase are described in AAW85672-W85678	
XX	XX		
SQ	Sequence	2558 BP; 750 A; 477 C; 592 G; 739 T; 0 U; 0 Other;	
Query Match			
Best Local Similarity		36.2%; Score 958.6; DB 2; Length 2558;	
Matches 1375; Conservative		0; Mismatches 604; Indels 24; Gaps 3;	
Qy	202	ATTTCATTATGGTCACAACTGATGCTTCAATGCTGATTTGGATTGTTGTCATGT 261	

Db 1327 CGATAGCTGATCTGTTGAATTTCTCCCAAGAGGCTGCTCTGCATGCTTTGGCTGCTTAT 1386
Qy 1339 GCAITCTGACCCAGTGAAGCAGAGAGATTTCGCGCTTTTGTGTCATCACTCTGGGAAGAAT 1398
Db 1387 GCATCCGATCCAAAGGAAGCGAGCGACTAAGGTATCTTCGCTCTCTCTGCTGGGAAGAC 1446
Qy 1399 GAGTATTCAAAATGGGTAGTGTGAAGTTCAGAGGAGTCTTTTGAGATCAAGCCGAGTTT 1458
Db 1447 GAATACGCCCAGTGATAGTAGCTAGTCAGAGAAGTCTGCTAGTGTTCATGGCTGAATTC 1506
Qy 1459 CCATCAGCAAAACCCCTCTTGGTGTGTTCTTTCGTCGAGTAGCCCTCGCTTACCGCCT 1518
Db 1507 CCATCAGCAAGGCTCCAAATGGGTTTCTTTGACAGCAGTAGCTCTCGTTGCTGCCA 1566
Qy 1519 CGATACATTTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCATGTGAGTGT 1578
Db 1567 AGATACTATTCTATTTTCATCTTCCAAATAGGATGGTACCATCTAGGATTCATGTCAATGT 1626
Qy 1579 GCTTTAGTATATGTCAAAGCCCTACCGGAAGGTTTCACCGAGGAGTGTTCGACATGG 1638
Db 1627 GCATTTGTGATGAAAAAACACCGGAGGTTCGCGGTTCACAAAGGAGTGTTCACCTGG 1686
Qy 1639 ATGAAGCATCAGTTCCTCAGGA-----TAGCTGGGCTCCTATTTTT 1680
Db 1687 ATGAAGAAATTCGTGTCTTTTGGGAAGAAACCATGATTCGACGAGCTGGGCACCAATCTTT 1746
Qy 1681 GTTCGAAGCTCAAACTCAAGTTACGAGTGAACCCCTCAACTCCAATTCATGTGGGGA 1740
Db 1747 GTCAGGCAATCCAACTTCAAACTTCCTGCTGATTTACAGTACCAATTAATGATTTGT 1806
Qy 1741 CTTGGTACAGGGTTAGTCTCTTTTCAGAGGATTTCTCAGGAAGAAGATGCCCTCAAGGA 1800
Db 1807 CTTGGGACTGGATAGTCTCCCTTTAGGGGATTCATGAGGAGGATTAGCTCTGAAGAAT 1866
Qy 1801 AATGGTGTCTCAACTGGCCCGACAGTGTCTTTTTCGGATGTAGGAATCGTAATATGGAC 1860
Db 1867 TCTGTGTAGAATTTGGGACCGCTATCCCTCTTTTGGATGCAGAAACAGACAGATGGAT 1926
Qy 1861 TTCAATTTAAGACGAACTAAACAACCTTCGTGGAACGAGGAGTCAATTCGGAGCTAGTT 1920
Db 1927 TACATATATGAAGAGGAGCTAAACAACCTTTGTGAAAGAGGAGCTATCTCCGAAGTTGTT 1986
Qy 1921 ATTGCCCTTTTCAGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGGAGAA 1980
Db 1987 GTTGCTTTCTCAGTGAAGGAGCTAACAGGAATACGTAACAATAAATGGCGGAGAAG 2046
Qy 1981 GCAACGATGTATCGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTATGCC 2040
Db 2047 GCTTCCTACATCTGGGAATGATCTCTCAAGGTGCTTATCTTTATGTATGTGTATGCC 2106
Qy 2041 AAGGGAATGCCAGAGATGCCATTCGACGCTTGATACCAATTCGCCAAGAAACAGGAGCC 2100
Db 2107 AAGGGATGGCTAGAGACGTACATCGAACTCTCCACACCATTCGCCAGGAACAGGGATCT 2166
Qy 2101 ATGGAATCATCTGCTCCGAGCTGCAGTAAGAACTCCAAGTTGAAGAACATATCTA 2160
Db 2167 TTGGACAACTCGAAGACCGGAAGCTTGGTGAAGAAATCTACAGATGGATGAAGGTATCTA 2226
Qy 2161 AGAGATGCTCTGGTGATCGAATGT 2183
Db 2227 CGTGATGTGGTGAATGATTTT 2249

RESULT 4

AAC44709

ID AAC44709 standard; DNA; 2136 BP.

XX AC AAC44709;

XX AC

XX AC

DT 18-OCT-2000 (first entry)

XX XX

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 43838.

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway; metabolic pathway;
promoter; termination sequence; ss.
Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-00301439.

25-FEB-1999; 99US-0121825P.

05-MAR-1999; 99US-0123180P.

09-MAR-1999; 99US-0123548P.

23-MAR-1999; 99US-0125788P.

25-MAR-1999; 99US-0126264P.

29-MAR-1999; 99US-0126785P.

01-APR-1999; 99US-0127462P.

06-APR-1999; 99US-0128234P.

08-APR-1999; 99US-0128714P.

16-APR-1999; 99US-0129845P.

19-APR-1999; 99US-0130077P.

21-APR-1999; 99US-0130449P.

23-APR-1999; 99US-0130510P.

23-APR-1999; 99US-0130891P.

28-APR-1999; 99US-0131449P.

30-APR-1999; 99US-0132048P.

30-APR-1999; 99US-0132407P.

04-MAY-1999; 99US-0132484P.

05-MAY-1999; 99US-0132485P.

06-MAY-1999; 99US-0132486P.

06-MAY-1999; 99US-0132487P.

11-MAY-1999; 99US-0132863P.

11-MAY-1999; 99US-0134256P.

14-MAY-1999; 99US-0134218P.

14-MAY-1999; 99US-0134219P.

14-MAY-1999; 99US-0134221P.

14-MAY-1999; 99US-0134370P.

18-MAY-1999; 99US-0134768P.

19-MAY-1999; 99US-0134941P.

20-MAY-1999; 99US-0135124P.

21-MAY-1999; 99US-0135353P.

24-MAY-1999; 99US-0135629P.

25-MAY-1999; 99US-0136021P.

27-MAY-1999; 99US-0136392P.

28-MAY-1999; 99US-0136782P.

01-JUN-1999; 99US-0137222P.

03-JUN-1999; 99US-0137528P.

04-JUN-1999; 99US-0137502P.

07-JUN-1999; 99US-0137724P.

08-JUN-1999; 99US-0138094P.

10-JUN-1999; 99US-0138540P.

10-JUN-1999; 99US-0138847P.

14-JUN-1999; 99US-0139119P.

16-JUN-1999; 99US-0139452P.

16-JUN-1999; 99US-0139453P.

17-JUN-1999; 99US-0139492P.

18-JUN-1999; 99US-0139454P.

18-JUN-1999; 99US-0139455P.

18-JUN-1999; 99US-0139456P.

18-JUN-1999; 99US-0139457P.

18-JUN-1999; 99US-0139458P.

18-JUN-1999; 99US-0139459P.

18-JUN-1999; 99US-0139460P.

18-JUN-1999; 99US-0139461P.

18-JUN-1999; 99US-0139462P.

18-JUN-1999; 99US-0139463P.

18-JUN-1999; 99US-0139750P.

21-JUN-1999; 99US-0139763P.

21-JUN-1999; 99US-0139817P.

22-JUN-1999; 99US-0139899P.

23-JUN-1999; 99US-0140353P.

```
PR 23-JUN-1999; 99US-0140334P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140931P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 18-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 23-JUL-1999; 99US-0145152P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.

PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 33.8%; Score 895.4; DB 3; Length 2136;
Best Local Similarity 67.3%; Pred. No. 8.7e-231;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

QY 206 TCATTATGTCACAACTGTAGCTTCAATGCTGATTGAGATTGGTTCTTCGCAATGATGA 265
DB 161 TGAATTGTTACCACTTCCATTGCTCTTATTGTTGTCATCGTTATGCTGTTTGGAGGA 220
QY 266 AATCTTTCGCTCTCTCAATCAAAACCTATTGAACTTATAAACCAATAATTGATAAAG 325
DB 221 GATCCGGTTCTGGGAATTCAAAACGTGCGAGCTCTTAAGCCTTTGGTTATTAAAGCCTC 280
QY 326 AAGAGGAGATTGAAGTTGATTCCTGGTAAATTAAGCTCACTATATATTTTGGTACTCAGA 385
DB 281 GTGAGGA---AGAGATTGATGATGGCGGTAAGAAAGTTACCACTCTTTTCGGTACACAAA 337
QY 386 CTGGTACTGCTGAAGGATTTCGCAATTAAGGCAAGAAATTAAGGCAAAAGTACACAGA 445
DB 338 CTGGTACTGCTGAAGGTTTTTGAAGGCTTTAGGAGAGAAGCTAAAGCAAGATATGAAA 397
QY 446 AAGCAGTTCTTAAAGTAGTTGACCTGGATGACTATGCACCGGAGGATGATCAATATGAAG 505
DB 398 AGACCAGATTCAAAATCGTTGATTTGGATGATTACCGCGCTGATGATGATGATGAGG 457
QY 506 AGAAATTAAGAAAGAGTCTTTTGGTGTCTTTTCATGCTAGCCACTTATGTTGATGGTGAGC 565
DB 506 AGAAATTAAGAAAGAGTCTTTTGGTGTCTTTTCATGCTAGCCACTTATGTTGATGGTGAGC 565
```


PT Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.

PS Claim 144; SEQ ID NO 803; 577bp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX Sequence 2136 BP; 595 A; 424 C; 519 G; 598 T; 0 U; 0 Other;

Query Match 33.8%; Score 895.4; DB 6; Length 2136;

Best Local Similarity 67.3%; Pred. No. 8.7e-231;

Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

206 TCATTATGGTCAACACTGTAGCTTCAATGCTGATTGGATTGGTTCTCGCATGTATGA 265
161 TGATTGTTACACTTCCATTGCTGTTCTTATGCTGTCATGCTGTTGGAGGA 220
266 AATCTTCGCTTCTCAATCAAAACCTATTGAACCTTATAACCAATTAATTGATAAGAG 325
221 GATCCGGTCTCGGAATTCAAAACGTCGAGCCTCTTAAGCCTTTGGTTATTAAAGCCTC 280
326 AAGAGGAGATTGAAGTTGATCTCGTAAATTAAGCTCACTATATTTTGGTACTCAGA 385
281 GTGAGGA---AGATTGATGATGGCGGTAAAGATTACATCTTTTCGGTACAAA 337
386 CTGCTACTGCTGAAGGATTTGCTAAGGCATTGGCAGAGAAATTAAGCCTAAGTACAAGA 445
338 CTGCTACTGCTGAAGGTTTTCGAAAGCTTTAGGAGAAGAGCTAAAGCAAGATATGAA 397
446 AAGCAGTTGTTAAAGTATGTCCTGATCACTATGACGCGGAGGATGATCAATATGAAG 505
398 AGACCAGATTCAAAATCGTTGATTGGATGATTAACGCGGCTGATGATGATGATGAGG 457
506 AGAAATTAAGAAAGAGCTCTTGGTGTCTTTCATGCTAGCCACTATGGTGTGCTGAGC 565
458 AGAAATTAAGAAAGAGATGTCGCTTCTTCTTCTTAGCCCATATGGAGATGGTGAGC 517
566 CAACGTCAATGCTGCGAGATTTTACAAATGGTTCACTCAGGAACATGAAGGGGAGAGT 625
518 CTACCGAATGCGCGAGATTTACAAATGGTTTCCAGGAGGGAATGACAGAGAGAAAT 577
626 GGCTTCAGCAACTAACTTATGCTGTTTGGTGGTAAACCGTCAATACGAGCATTTCA 685
578 GGCTTAAGAACTTGAAGTATGAGTGTGTTGGATTAGGAAACAGACAATATGACCAATTTA 637
686 ACAAGATCGCGGTAGATGTCGATGAGCACTCCGTAACAGGTGCAAGCGCATTTGTC 745
638 ATAAGGTTGCAAGTTGTAGATGACATCTCTGCGAAACAAAGGTGACAGCGCTTTGTAC 697
746 AAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTTGGCGAGAA 805
698 AAGTGGCTTTGGAGATGATGACGAGTGTATTGAAGTACTTTACGCTTGGCGAGAG 757
806 TGTGTGGAATGAAATGATGATGCTTCAAGATGAGGATGCTGCTCTTCAAGTGGCTA 865
758 CATTTGGCCCGAGCTTGTATCAATACTGAGGGAAGAAAGGGGATACAGCT---GTTGCCA 814
866 CACCGTATATTTGCTACTGTTCTCTGAAATACAGGCTAGTATTACGAAACTACGGTCCGG 925
815 CACCATACACTGCGAGCTGTTTGAATATACAGAGTTTCTATTACGACTCTGAAGATGCCA 874
926 CTCTGGATGATAAACACATAAATACTGCTAAACGGCGATGTTGCATTTGATATTCTCCATC 985

875 AATTCAATGATATAACATCGCAATGGGAATGGTACATCTGTTTGTATGCTCAACATC 934
986 CTTGAGAACCAATGTTGCTCAACAAGAGAGAGCTCCAAACCAAGCTGTGATAGATCCT 1045
935 CTTTCAAAAGCAAAATGTCGCTGTTTAAAGGGAGCTTCACTATCTCCGAGCTGTGCTCTT 994
1046 GTATACATCTGGAGTTGCGACATATAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
995 GTATCCATTTGGAATTTGACATTTGCTGGAAGTGAATTCATGATGAAACTGGAGATCATG 1054
1106 TTGGTGTGTTATGCTGGAACCTGCGATGAAACTGTGAGGAAGCAGGGAAGCTGTTGGGTC 1165
1055 TTGGTGTGTTATGCTGTAACCTTAAGTGAATACTGTAGATGAAGCTCTTGTAGATTGCTGGATA 1114
1166 AACCCCTGGATTTGCTGTTTCAATTCACAGGATAAAGAGAGCGGTCAACCCAGGGAA 1225
1115 TGTACCTGATATCTTATTTCTCAGCTGAAAAAAGAGACGGCACCAATCAGCA 1174
1226 GCTCATTTACCACCTCTTTCCAGGTCCTTGACCTTTACGATCTGCCCTAGCACGCTATG 1285
1175 GCTCAGTCCCTCTCTCCCTTCCCA---CCTTGGCAACTTGAACAGCGCTTACAGATATG 1231
1286 CTGATCTTTTGAATCTCTCTAGAAAGCTTCTCTGATTGCTCTGTCCGCTCATGCACTCTG 1345
1232 CATGCTCTTTGAGTCTCTCAAGAGAGTCTGCTTTAGTTGGTGGCTGCTCATGCACTCTG 1291
1346 TACCCAGTGAAGCAGAGAGATTCGGCTTTTGTGTCATCACCTCTGGGAAAGAAATGAGTATT 1405
1292 ATCTTACCGAAGCAGAACGATTAACACACCTTCTTCACTGCTGGAAGAGATGAATATT 1351
1406 CAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG 1465
1352 CAAAGTGGGTAGTAGAGATCAAGAGATCTACTTGAGGTGATGGCCGAGTTTCTCTTCTCAG 1411
1466 CAAAACCCCTCTTTGGTGTGTTCTTTGCTGAGTAGCCCTCGCTTACCCGCTCGATACT 1525
1412 CCAAGCCACCACTTGGTGTCTTCTCGTGGAGTGTCTCCCAAGGTGCGACGCTAGGTTCT 1471
1526 ATTCTATCTCATCTCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTGCTTTAG 1585
1472 ATTCGATATCATCATCCCAAGATTTGCTGAAACTAGAAATTCACGTACATGTGCACTGG 1531
1586 TATATCGTCAAAAGCCCTACCGAAGGTTTCAACGAGAGGTGCTCGACATGATGAAGC 1645
1532 TTTATGAGAAATGCGCAACTGGCAGGATTTCAAGGAGGTGTGTTCCACTTTGGATGAAGA 1591
1646 ATGCACTCTCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACGT 1690
1592 ATGCTGTGCTTACGAGAGAGTGAATACTGTTCTCGGCGCGATATTTGTTAGGCAAT 1651
1691 CAACTTCAAGTTACAGCTGACCCCTCAACTCAATTTATCTGTTGGGACCTGGTACAG 1750
1652 CCAACTTCAAGCTTCTCTGATTTCTAAGGTACCGATCATCATCGGTCGAGGAGCTG 1711
1751 GGTAGCTCTCTTTCAGAGGATTTCTGACGAAAGATGSCCTCAAGGAAATGTCGCTC 1810
1712 GATTGCTCATTCAGAGGATTCCTTCAGAAAGACTAGCGTTGGTAGAATCTGGTGTG 1771
1811 AACTTGGCCCGCAGAGTGTCTTTTTCGGATGTAGGAATCGTAAATATGCACTTCATTTATG 1870
1772 AACTTGGCCCATCAGTTTGTCTTCTTGGATGCAAGAACCGTAGAATGATTTTCATCTACG 1831
1871 AAGACAACTAAACAACTTCTGTTGGAACGAGGAGTCAATTTCCGAGCTAGTATTATTCCTTTT 1930
1832 AGGAAGAGCTCCAGCGATTTGTTGAGAGTGGTCTCTCGCAGAGCTAAAGTGTGCGCTTCT 1891
1931 CAGCTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGGAGAAAGCAACGATG 1990
1892 CTCTGAGAGAACCCCAAGAAATACGTACAGCAAGATGATGGACAGGCTTCTGATATA 1951
1991 TATGGAATGTGATATCAGGGGAGCGGTTATCTCTATGTGTGTGATGCCAAGGAATGG 2050

Db 1952 TCTGGAATATGATCTCTCAAGSAGCTTATTTATATGTTTGTGTGACGCCAAAGGCATGG 2011
QY 2051 CCAGAGATGTCCTCGACGCTTGCATACCATTCGCCAAGAACAGGACCCCATGGAATCAT 2110
Db 2012 CAGAGATGTTTCAAGATCTCTCCACACATAGCTCAAGAACAGGGGTCAATGGATCAA 2071
QY 2111 CTCTGCCGAAGTGCAGTAAAGAACTCCAAAGTTGAAGAACGATATCTTAAGAGATGTCT 2170
Db 2072 CTAAGAGCAGAGGGCTTCGTGAAGATCTGCAACCGAGTGAAGATATCTTAGAGATGTAT 2131
QY 2171 GGTGA 2175
Db 2132 GGTA 2136

RESULT 6
ADA68489
ID ADA68489 standard; DNA; 2136 BP.
XX
AC ADA68489;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 605.
XX
KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS Arabidopsis thaliana.
XX
PN W02003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 605; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2136 BP; 595 A; 424 C; 519 G; 598 T; 0 U; 0 Other;

Query Match 33.8%; Score 895.4; DB 8; Length 2136;
Best Local Similarity 67.3%; Pred. No. 8.7e-231;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

QY 206 TCATTATGGTCACAACGTAGCTTCAATGCTGATGGATTGGTTTCTTCGCAATGATGA 265
Db 161 TGATTGTTACCACTTCCATTGCTGTTCTTATTGGTTGCATCGTTATGCTCGTTTGGAGGA 220
QY 266 AATCTTCGTTCTTCAATCAAAACCTATTGAAACCTTATAAACCAATATTGATAAAGAG 325

Db 221 GATCCGGTCTCGGAATTCAAAACCGTGTGAGCCTCTTAAGCCTTTGGTTATTAAGCCTC 280
QY 326 AAGAGGAGATTGAGTTGATCTGTGTAATAAATTAAGCTCACTATATTTTGGTACTCAGA 385
Db 281 GTGAGGA---AGAGATTGATGATGGGCGTAAGAAGTTTACCATCTTTTTTCGGTACAAAA 337
QY 386 CTGGTACTCTGAAGGATTTGCTTAAGGCATTTGGCAGAGAAAATTAAGGCAAAAGTACAAGA 445
Db 338 CTGGTACTCTGAAGGTTTTTGCAGAGCCTTTAGGAGAGCAAGCTAAGCAAGATATGAAA 397
QY 446 AAGCAGTTGTTAAAGTAGTTGACCTCGGATGACTATGACAGCCGAGGATGATCAATATGAAG 505
Db 398 AGACCAGATTCAAAATCGTTGATTTTGGATGATTTACGCGGCTGATGATGATGATGAGG 457
QY 506 AGAAATTAAGAGAAAGAGTCTTTTGGTGTGTTTTCATGTGTAGCCACTTATGTGTGTTGAGC 565
Db 458 AGNAATTGAAGAAAGAGGATGTGGCTTCTTCTTAGCCACATATGGAGATGGTGAGC 517
QY 566 CAACTGACAAATGCTGCGAGATTTTACAAATGGTTTCACTCAGGAACATGAAAAGGGGAGAGT 625
Db 518 CTACCGACAAATGCAGCGAGATTTCTACAAATGGTTTCCACCGAGGGGAATGACAGAGGAGAAT 577
QY 626 GGCCTCAGCAACTAATCTTATGGTGTGTTTGGTAAACCGTCAATACGAGCATTTCA 685
Db 578 GGCCTTAAGAACTTGAAGTATGGAGTGTGTTGGATTTAGGAAACAGACAATATGAGCATTTTA 637
QY 686 ACAAGATCCGGTAGATGAGCAACTCGGTAACAAAGGTGCAAAAGCGCATTTGTTTC 745
Db 638 ATAAGTTGCCAAAGTTGTAGATGACATTTCTTGTGCAACAGGTGCACAGCGTCTTGATC 697
QY 746 AAGTGGGCTCGGTGACGATGATCAATGCAATTGAAGATGATTTTACTGCTTGGCGAGAAT 805
Db 698 AAGTTGGTCTTGGAGATGATGACCAAGTGTATTGAAGATGACTTTTACCGCTTTGGCGAGAAG 757
QY 806 TGTGTGGAATGAAATTTGGATCAGTTGCTCAAGATGAGGATGCTGCTCTTCACTAGTGGCTA 865
Db 758 CATTTGGCCCCGAGCTTGTATACAACTAGGGAAGAGGGGATACAGCT---GTTGCCA 814
QY 866 CACCGTATATTGCTACTGTTCTCTGAATACAGGGTAGTGTATTCACGAAAATCTACGGTCGCGG 925
Db 815 CACCATACACTGCAGCTGTGTTAGATACAGAGTTTCTATTACAGACTCTGAAGATGCCA 874
QY 926 CTCTGATGATAAACACATATAATGCTTAACGGCGATGTTGCAATTTGATATTTCTCATC 985
Db 875 AATTCAATGATATAAACATGCGCAAAATGGGAATGGTTTACACTGTGTTTGTATGCTCAACATC 934
QY 986 CTGCGAGAACCATTTGTTGCTCAACAAAGAGAGCTCCACAAACCCAGTCTGTATAGATCCT 1045
Db 935 CTTACAAAGCAATGTGCTGTGTTAAAGGGAGGCTTCATACTCCCGAGTCTGATCGTTCTT 994
QY 1046 GTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
Db 995 GTATCCATTTGGAATTTGACATTTGCTGGAAGTGGACTTACGTTATGAACTGGAGATCATG 1054
QY 1106 TTGGTGTATTGCTGAGAACTGCGATGAAACTGTGCGAAGCAGGGAAGCTGTTGGGTC 1165
Db 1055 TTGGTGTACTTTGTGATAACTTAAAGTGAACCTGTAGATGAAGCTCTTAGATTGCTGGATA 1114
QY 1166 AACCCCTGGAATTTGCTGTTTTCNAATTCACCGGATAAAGACGGGTCAACCCAGGGAA 1225
Db 1115 TGTCACTGTATACTTATTTTCTCACTTCACGCTGAAAGAACGCGCACCAATCAGCA 1174
QY 1226 GGTCAATTACCACTCTCTTTCCAGGTCCTTTGACACCTTACGATCTGCCCTAGCACGCTATG 1285
Db 1175 GCTCACTGCTCTCTCTCTTCCCA---CCTTGCAACTTTGAGAACAGCGCTTACACGATATG 1231
QY 1286 CTGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATTTGCTGCTCCGCTCATGTCATCTG 1345
Db 1232 CATGTCTTTTGTAGTTCTCCAAAAGAGTCTGCTTTTGTAGTTGGTGTGCTCATGTCATCTG 1291
QY 1346 TACCCAGTCAAGCAGAGATGGCGCTTTTGTGTCATCACCTCTGCGGAAGAAATGAGTATT 1405

```
Db 1292 ATCTACCGAAGCAGAACGATTAAACACACCTTGCTTCCACCTGCTGGAAGGATGAATATT 1351
Qy 1406 CAAAATGGTAGTGGAGTCAGAGGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG 1465
Db 1352 CAAAGTGGTAGTAGAGTCAAGAAAGTCTACTTGGAGTGATGGCCGAGTTTCCCTTCAG 1411
Qy 1466 CAAAACCCCTCTTTGGTGTGTTCTTTGCTGCAGTAGCCCTCGCTTACCGCCTCGATACT 1525
Db 1412 CCAAGCCACCATTTGGTGTCTTCTTCTGCTGAGTGTCTCCAGGTTGCAGCTAGTTCAT 1471
Qy 1526 ATTCTATCTCATCTCTCCCTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTCTTAG 1585
Db 1472 ATTCTGATATCATCTCCCAAGATCTCTGAAACTAGAAATTCAGTCCACATGTGCATGG 1531
Qy 1586 TATATGTCAAGCCCTTACCGAAGGTTCCAGGAGAGTGTTCGACATGATGAAGC 1645
Db 1532 TTATGGAATGCGCAACTGCGAGGATTCATAGGAGTGTGTTCACCTTGGATGAAGA 1591
Qy 1646 ATGAGTCTCTCAGGA-----TAGCTGGGCTCCTATTATTTTTCGAACGT 1690
Db 1592 ATGCTGTGCTTACGAGAAGTGAACCTGTTCTCGGCGCGATATTGTTAGGCAAT 1651
Qy 1691 CAACTTCAAGTTACAGCTGACCCCTCAACTCAATATCATGTGGGACCTGGTACAG 1750
Db 1652 CCAACTTCAAGCTTCTCTCTGATTCTAAGGTACCGATCATCATCGTCCAGGGACTG 1711
Qy 1751 GGTAGTCTCTTCAGAGGATTTCTGCAGAAAGATGGCCCTCAAGGAAATGGTCTC 1810
Db 1712 GATTAGTCTCAATCAGAGGATTCCTTCAGAAAGACTAGCGTTGGTAGAATCTGGTGTG 1771
Qy 1811 AACTTGGCCCGCAGCAGTCTCTTTTCGATGTAGGAATCGTAATATGGAATTCATTATG 1870
Db 1772 AACTTGGCCATCAGTTTGTCTTTGGATGCAGAAACCGTAGAATGGATTTCATCTAG 1831
Qy 1871 AGACGAACCTAAACAATCTCGTGGAGAGGATCTATTTTCGGAGTAGTTATTGCCCTTT 1930
Db 1832 AGAAGAGCTCCAGCGATTTGTTGAGAGTGGTCTCTCGCAGAGCTAAGTGTCCCTTCT 1891
Qy 1931 CAGTGAAGGGAAAGAGGATATGTTCAACATAGATGATGGAGCAACGAGATG 1990
Db 1892 CTGTAAGAGCCCAACAAAGATACGTACAGCACAAGATGATGGACAGGCTTCTGATA 1951
Qy 1991 TATGGAATGTGATATCAGGGGCGGTTATCTATGTGTGTGTGTATGCCAAGGGAATGG 2050
Db 1952 TCTGGAATATGATCTCTCAGGAGCTATTATATGTTGTGTGTGTGACCCAAAGGATGG 2011
Qy 2051 CCAGAGATGCCATCGCAGCTTGCATACCATTCGCCAAGAACAGGACCCATCGAATCAT 2110
Db 2012 CAAGAGATGTTTCAAGATCTCTCCACAAATAGCTCAAGAACAGGGGTCAATGGATTCAA 2071
Qy 2111 CTGCTCCGAGCTGCAGTAAGAAATCCCAAGTTGNAAGACCATATCTAAGAGATGTCT 2170
Db 2072 CTAAGCAGAGGGCTTCGTGAAGATCTCGAAACGATGGAAGATATCTTAGAGATGTAT 2131
Qy 2171 GGTGA 2175
Db 2132 GGTAA 2136

RESULT 7
AAQ51237
ID AAQ51237 standard; cDNA; 2423 BP.
XX AC AAQ51237;
XX DT 25-MAR-2003 (revised)
XX DT 11-MAY-1994 (first entry)
XX DE Plant NADPH cytochrome P450 reductase (ara C).
XX KW NADPH cytochrome P450 reductase; functional complementation;
XX KW identification; ss.

OS XX Arabidopsis thaliana.
PH FT Key Location/Qualifiers
FT CDS 131..2269
FT /tag= a
FT /product= "NADPH cytochrome P450 reductase."
FT misc_difference 374..376
FT /tag= b
FT /transl_except= CGT encodes Lys.
FT misc_difference 410..412
FT /tag= c
FT /transl_except= CGT encodes Lys.
FT misc_difference 434..436
FT /tag= d
FT /transl_except= CGT encodes Lys.
FT misc_difference 518..520
FT /tag= e
FT /transl_except= AGA encodes Lys.
FT misc_difference 665..667
FT /tag= f
FT /transl_except= AGA encodes Lys.
FT misc_difference 698..700
FT /tag= g
FT /transl_except= AGA encodes Lys.
FT misc_difference 749..751
FT /tag= h
FT /transl_except= AGA encodes Lys.
FT misc_difference 818..820
FT /tag= i
FT /transl_except= CGT encodes Lys.
FT misc_difference 881..883
FT /tag= j
FT /transl_except= CGA encodes Lys.
FT misc_difference 917..919
FT /tag= k
FT /transl_except= AGG encodes Lys.
FT misc_difference 974..976
FT /tag= l
FT /transl_except= AGA encodes Lys.
FT misc_difference 1091..1093
FT /tag= m
FT /transl_except= AGG encodes Lys.
FT misc_difference 1118..1120
FT /tag= n
FT /transl_except= CGT encodes Lys.
FT misc_difference 1232..1234
FT /tag= o
FT /transl_except= AGA encodes Lys.
FT misc_difference 1340..1342
FT /tag= p
FT /transl_except= AGA encodes Lys.
FT misc_difference 1355..1357
FT /tag= q
FT /transl_except= CGA encodes Lys.
FT misc_difference 1439..1441
FT /tag= r
FT /transl_except= CGA encodes Lys.
FT misc_difference 1583..1585
FT /tag= s
FT /transl_except= AGG encodes Lys.
FT misc_difference 1595..1597
FT /tag= t
FT /transl_except= AGG encodes Lys.
FT misc_difference 1637..1639
FT /tag= u
FT /transl_except= AGA encodes Lys.
FT misc_difference 1684..1686
FT /tag= v
FT /transl_except= AGG encodes Lys.
FT misc_difference 1763..1765
FT /tag= w
FT /transl_except= CGG encodes Lys.
FT misc_difference 1778..1780
```



```

FT FT /*tag= x
FT FT /transl_except= AGG encodes Lys.
FT FT misc_difference 1859..1861
FT FT /*tag= y
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 1877..1879
FT FT /*tag= z
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 1937..1939
FT FT /*tag= aa
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 1943..1945
FT FT /*tag= ab
FT FT /transl_except= CGT encodes Lys.
FT FT misc_difference 1946..1948
FT FT /*tag= ac
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 1979..1981
FT FT /*tag= ad
FT FT /transl_except= CGA encodes Lys.
FT FT misc_difference 2027..2029
FT FT /*tag= ae
FT FT /transl_except= CGT encodes Lys.
FT FT misc_difference 2147..2149
FT FT /*tag= af
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 2159..2161
FT FT /*tag= ag
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 2246..2248
FT FT /*tag= ah
FT FT /transl_except= AGA encodes Lys.
FT FT misc_difference 2255..2257
FT FT /*tag= ai
FT FT /transl_except= AGA encodes Lys.
XX XX
PN W09321326-A2.
XX XX
PD 28-OCT-1993.
XX XX
XX 13-APR-1993; 93WO-FR000367.
XX XX
PR 13-APR-1992; 92FR-00004491.
XX XX
PA (ORSA-) ORSAN.
XX XX
PI Kazmaier M, Lacroute F, Mignotte-Vieux C, Minet M, Pompon D;
XX XX
DR WPI; 1993-351736/44.
DR P-PSDB; AAR43582.
XX XX
PT New DNA encoding plant NADPH cytochrome P450 reductase - cloned by
PT functional complementation in yeast, also recombinant enzyme useful in
PT P450 mediated bioconversion processes.
XX XX
PS Claim 11; Fig 10; 79pp; French.
XX XX
CC A new method for determining whether a DNA sequence encodes an NADPH
CC cytochrome P450 reductase involves transforming yeasts with plasmids of a
CC total cDNA bank of plant(s). The yeasts used in the procedure are
CC incapable of producing their own NADPH cytochrome P450 reductase. They
CC are then exposed to a cytochrome P450 inhibitor at a level which is
CC lethal to the yeast cells but not to cells which, because of the
CC transformation, now contain an active NADPH cytochrome P450 reductase.
CC Surviving clones are then isolated and plasmid DNA extracted. The gene is
CC inserted into the plasmid at a site which places it under the control of
CC an inducible promoter. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
SQ Sequence 2423 BP; 674 A; 497 C; 552 G; 700 T; 0 U; 0 Other;
Query Match 33.0%; Score 875; DB 2; Length 2423;
Best Local Similarity 66.5%; Pred. No. 3e-225;
Matches 1326; Conservative 0; Mismatches 640; Indels 27; Gaps 4;

```

```

QY 206 TCATTATGTCACAACTGTAGCTTCAATGCTGATGGATTTGGTTTCCTCGCATGTATGA 265
DB 291 TGAATGTTACCACTTCCATTGCTGTTCTTAATGGTTGCATCGTTATGCTCGTTGGAGGA 350
QY 266 AATCTTCGCTTCTCAATCAAAAACCTATTGAACCTTATAAACCATAATATGATAAGAAG 325
DB 351 GATCCGGTTCTCGGAATTCAAAACGTCGAGCCCTCTTAAGCCTTTGGTTATTAAGCCCTC 410
QY 326 AAGAGGAGATTGAAGTTGATCCTGGTAAATTAAGCTCACTATATATTTTGGTACTCAGA 385
DB 411 GTGAGGA---AGAGATTGATGATGGCGGTAAAGAAATTAACCATCTTTTCGGTACACAAA 467
QY 386 CTGCTACTGCTCAAGGATTTGTAAAGCATTTGGCAGAGAAATTAAGGCAAAAGTACAAGA 445
DB 468 CTGCTACTGCTCAAGGTTTTCGCAAGGCTTTAGGAGAGAAAGCTAAAGCAAGATATGAAA 527
QY 446 AAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCGGAGGATGATCAATATGAAG 505
DB 528 AGACCAGATTCAAAATCGTTGATTTGGATGATTAACGCGCTGATGATGATGATGAGG 597
QY 506 AGAAATTAAGAGAAAGAGTCTTTGGTGTCTTTTCATGCTAGCCACTTATGCTGATGGTGAGC 565
DB 588 AGAATTTGAAGAAAGAGGATGTGGCTTCTTCTTCTTAGCCACATATGAGATGGTGAGC 647
QY 566 CAACCTGACAATGCTCGAGATTTTACAATGTTTCACTCAGGAAACATGAAAGGGGAGAGT 625
DB 648 CTACCGACAATGCAGCGAGATTTCAAAATGTTTACCAGGGGGAATGACAGAGAGAAAT 707
QY 626 GGCTTCAGCAACTAACTTATGCTGTTTGGTAAACCGTCAATCAGGAGCATTTTCA 685
DB 708 GGCCTTAAGAACTTGAAGTATGGAGTGTGGGATTAGGAAACAGACAAATATGAGCATTTTA 767
QY 686 ACAAGATCGCGGTAGATGTGAGTGAACCACTCGGTAAACAAAGGTGCAAAAGCGCATTTGTC 745
DB 768 ATAAGGTTGCCAAAGTTGTAGATGACATTTCTTGTGCGAACAAAGTGCACAGCGTCTGTAC 827
QY 746 AAGTGGGCTCGGTGACGATGATCAATGATTTGAAGATGATTTTACTGCTGGCGAGAAAT 805
DB 828 AAGTTGGTCTTGGAGATGATGACCAAGTGTATTTGAAGATGACTTTTACCGCTTGGCGAGAA 887
QY 806 TGTGTGGACTGAATTTGGATCAGTTGCTCAAAAGATGAGGATGCTGCTCTTCAGTGGCTA 865
DB 888 CATTTGGCCCGAGCTTGAATCAATCTGAGGGAAGAGGGGATACAGCT---GTTGCCA 944
QY 866 CACCGTATATTGCTACTGTTCTCTGAATACAGGGTAGTGATTCACGAAACTACGGTCGGG 925
DB 945 CACCATACACTCGAGCTGTGTTAGAATACAGAGTTTCTATTACGCACTCTGAAGATGCCA 1004
QY 926 CTCTGGATGATAAACACATATAATCTGCTAAACGGGATGTTGATTTGATATTTCTCATC 985
DB 1005 AATTCAATGATATAACATTTGGCAATGGGAATGGTTTACACTGTGTTGTGATGCTCAACATC 1064
QY 986 CTTGCGAGACCAATGTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGATAGATCCT 1045
DB 1065 CTTACAAAGCAATGTCGCTGTTAAAGGGAGGCTTCATACTCCGAGTCTGATCGTTCTT 1124
QY 1046 GTATACATCTGAGATTGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
DB 1125 GTATCCATTTGAAATTTGACATTCGTGGAAGTGGACTTACGATGAAACTTGGAGATCATG 1184
QY 1106 TTGGTGTATTGCTGAGAACTCGGATGAACCTGTCGAGGAAGCAGGGAAGCTGTTGGGTC 1165
DB 1185 TTGGTGTACTTTGTGATAACTTTAAGTGAACCTGTAGATGAAGCTCTTAGATTGCTGGATA 1244
QY 1166 AACCCCTGATTTGCTGTTTTCAAATTCACCGGATAAAGAACGGGTCAACCCAGGGAA 1225
DB 1245 TGTACCTGATATCTATTCTCTTCACTTCAAGGATGAAAGAGCGGCACCAATCAGCA 1304
QY 1226 GTCATTATACCACCTCTCTTCCAGGTCCTTGCACCTTACGATCTGCGCTTAGCACGCTATG 1285
DB 1305 GCTCACTGCTCTCTCTTCCCA---CCTTGCAACTTGAGAACAGCGCTTACACGATATG 1361

```


QY 923 CGGCTCTGGATGATAACACATAAATACTCTCTAACCGCGAGTTGGTTCATTTGATATTTCTCC 982
Db 942 CAACTGTGGACGAAAGAACAGCAGCTTAATGGAATGGCCATCTGTGTGGACGCTCATC 1001
QY 983 ATCCTTGCAGAACCATTTGTTGCTCAACAAAGAGAGCTCCACAAACCCAGTCTGATAGAT 1042
Db 1002 ATCCAGTCAGGGCTAATGTGGCTGTGCGAAAGAGCTTCATCTCTGCATCAGATCGTT 1061
QY 1043 CTTGTATACATCTGGAGTTCCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATC 1102
Db 1062 CTTGCACTCATTTAGAAATTTGACATTTAGGACACCGAGTTGTATATGAAACAGGGGACC 1121
QY 1103 ATGTTGGTGTATGCTGAGAACTGGATGAATCTGTGAGAGAAAGCAGGGAAGCTTTGG 1162
Db 1122 ATGTTGGTGTATGCTGAGAAATTTATCCGACATCTGTGGAAGAGGAGGAAAGGATAGTAG 1181
QY 1163 GTCAACCCCTGGATTTGCTGTTTCAATTCACACGGATAAAGAGACGGTCAACCCAGG 1222
Db 1182 GTTTGTCGCCGGAACACTATTTCTCCGTCCATACCGATGACGAAGATGGGAAACCTCTTG 1241
QY 1223 GAAGCTCATPACCACTCTCTTCCAGGTCCTTGCACCTTACCGATCTGCCCTAGCACGCT 1282
Db 1242 GTGGAAGCTCTTGGCTCTCTCTTCCACCCCTGTACTTTAAGAACAGCGCTTGCTAAAT 1301
QY 1283 ATGCTGATCTTTGAATCTCTCTAGAAAGCTTCTCTGATGCTCTGTGCGCTCATGCAT 1342
Db 1302 ACGCAGATGTTTGGAGTTCACTTAAAGAGTCTGCTTGGCTTAGCTGTCTCATGCAT 1361
QY 1343 CTGTACCCAGTGAAGCAGAGAGATGCGCTTTTGTGCATCACCTCTGGGAAAGAAAGT 1402
Db 1362 CTGATCCATCTGAAGCGGATCGATAGACATCTTGCTCACCCTGCTGGAAGGATGAGT 1421
QY 1403 ATTCAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCGAGTTTCCAT 1462
Db 1422 ATGCAGATGGGTGATTTGCCCTCTCAAGAGTCTCTTGAGGTATGSGCTGAATTTTCAT 1481
QY 1463 CAGCAAAACCCCTCTTGGTGTTCTTGTGTCAGTAGGCCCTCGCTTACCGCCCTCGAT 1522
Db 1482 CAGCCAAACCTCCAATTTGGTGTCTTTTGTGCATCAGTTGCTCTCGCTACAGCCAAAGT 1541
QY 1523 ACTATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTGCTT 1582
Db 1542 ATTATTCAAATTCATCATCTCAAGAGTGGCACCATCCAGAAATTCATGTACCTGCGCGT 1601
QY 1583 TAGTATATGTTCAAAGCCCTACCGAAGGGTTTCAACGAGGAGTGTGTTCCACATGGATGA 1642
Db 1602 TAGTGCATGATAAAATGCCACTGGACGGATTTCATCAAGGAGTGTGTTCAACTTGGATGA 1661
QY 1643 AGCATGAGTTCTCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAA 1687
Db 1662 AGAATTTCTGCACCAATTTGGGAAAGTCAGGACTGTAGTTGGGCTCCTATCTTTGTTAGGC 1721
QY 1688 CGTCAAACTTCAAGTTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGACCTGGTA 1747
Db 1722 AGTCCAAATTCAGACTCCCTGCTGATTAATAAGTGCCTATAATATGATAGTGCTGSCA 1781
QY 1748 CAGGGTTAGCTCCTTTTTCAGAGGATTTCTGCAGAAAGAAATGGCCCTCAAGGAAATTTGGTG 1807
Db 1782 CTGGTTGGCTCTTTCAGAGGTTTCTTGCAGGAAGATAGTCTTTGGAAGAGAGAGAG 1841
QY 1808 CTCAACTTGGCCAGCAGTCTCTTTTTCGGATGTAGGAATCTGAATATGGAATTCATTT 1867
Db 1842 CTGAGCTAGGCCCTCTGTGTTTATCTTTGTTGTCAGGAACCGTCAAGTGGACTATATCT 1901
QY 1868 ATCAAGACGAACATAAACAATCTCGTGGAAAGAGAGTCTATTTTCGGAGCTAGTTATTGCCT 1927
Db 1902 ACCAAGATGAAATGAAACCATTTCTGTCATGGTGGCGCACTTTCTGAGCTCATTTGTCCT 1961
QY 1928 TTTTCAGTGAAGGGGAAAGAAAGAAATATGTTTCAACATAGATGATGGGAAGCAACGG 1987
Db 1962 TCTCAGCAGAGGGGCTCTACTAGGAATATGTCTCAACATATAAATGATGAGAGAGGCTTCAG 2021

QY 1988 ATGTATGGAATGTGATATATCAGGGACGGTTATCTCTATGTGTGTGTGTATGCCAAGGAA 2047
Db 2022 ATATTGGAAACATGATATCTCAGGGAGCTTACATTTATGTGTGTGTATGCCAAGGTA 2081
QY 2048 TGGCCAGAGATGTCCATCGCAGCTTGCATACCATTCGCCCAAGAACAGGACCCCATGGAAT 2107
Db 2082 TGCTTAGATGTACACCGCACTCTACATACAAATTTTGAAGAACAGGCGTCTTTGGACA 2141
QY 2108 CATCTGCTCCGAAAGCTGCAGTAAGAAACTCCAAGTTGAAGAACGATATCTAAGAGATG 2167
Db 2142 ATTCCAAGACTCAGAGCATGGTTAAGAACCTACAAATGACTGGCAGATATTTCGCGTATG 2201
QY 2168 TCTGTGTAT 2176
Db 2202 TATGGTAAT 2210
RESULT 10
AAD33078
ID AAD33078 standard; DNA; 1863 BP.
XX
AC AAD33078;
XX
DT 01-JUL-2002 (first entry)
XX
DE Helianthus tuberosus cytochrome p-450 reductase DNA.
KW Para-hydroxycinnamic acid; PHCA; food packaging; electronic connector;
KW phenylalanine ammonia lyase; PAL; glucose; tyrosine ammonia lyase; TAL;
KW cytochrome p-450; cytochrome p-450 reductase; liquid crystal polymer;
KW LCP; telecommunication; medical device; aerospace application; enzyme;
KW biocatalyst; gene; ds.
XX
OS Helianthus tuberosus.
FH
FT Key Location/Qualifiers
CDS 1..1767
FT /*tag= a
FT /product= "Helianthus tuberosus cytochrome p-450
FT reductase"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN WO200210407-A1.
PD
PD 07-FEB-2002.
XX
PF 23-JAN-2001; 2001WO-US002099.
XX
PR 27-JUL-2000; 2000US-00627216.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Gatenby AA, Sariaslani FS, Tang X, Qi WW, Vannelli T;
XX
XX WPI; 2002-280635/32.
DR P-PSDB; AAE20656.
XX
XX Novel nucleic acid encoding truncated mutant tyrosine ammonia lyase (TAL)
PT polypeptide, or mutant TAL polypeptide, useful for producing
PT parahydroxycinnamic acid in recombinant host cell lacking cinnamate
PT hydroxylase.
XX
XX Example 6; Page 106-109; 139pp; English.
XX
XX The invention relates to methods for biological production of para-
CC hydroxycinnamic acid (PHCA). The invention relates to developing of a new
CC biocatalyst for conversion of glucose to PHCA by incorporation of the
CC wild type phenylalanine ammonia lyase (PAL; EC 4.3.1.5) from the yeast
CC Rhodotorula glutinis into Escherichia coli underlying the ability of the
CC wildtype PAL to convert tyrosine to PHCA. The invention is also directed
CC to developing a new biocatalyst for conversion of glucose to PHCA by
CC incorporation of the wildtype PAL which possesses enhanced tyrosine


```
DE Helianthus tuberosus cytochrome P-450 reductase enzyme DNA.
XX
KW Phenylalanine ammonia-lyase; PAL; enzyme; cinamate; food packing; PHCA;
KW para-hydroxycinnamic acid; tyrosine ammonia-lyase; TAL; medical device;
KW Liquid Crystal Polymer; LCP; electronic connector; Jerusalem artichoke;
KW aerospace application; cytochrome P-450 reductase; telecommunication;
KW chemical; db.
XX
OS Helianthus tuberosus.
XX
FH Key Location/Qualifiers
FT 1..1767
FT CDS
FT
FT /product= "H. tuberosus cytochrome P-450 reductase"
FT /note= "CDS does not include start codon"
FT /partial
XX
PN W0200111071-A2.
XX
XX 15-FEB-2001.
XX
XX 03-AUG-2000; 2000WO-US021156.
XX
XX 06-AUG-1999; 99US-0147719P.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Tang X, Vannelli TM, Qi WW, Sariaslani S, Gatenby AA;
XX WPI; 2002-121549/16.
XX P-PSDB; AAE16392.
XX
XX Producing para-hydroxycinnamic acid for producing liquid crystal polymer,
XX comprises converting cinamate to PHCA, glucose to PHCA by phenyl ammonia
XX -lyase route, or generating a biocatalyst with tyrosine ammonia-lyase
XX activity.
XX
XX Claim 20; Page 73; 75pp; English.
XX
XX The invention relates to a method for producing para-hydroxycinnamic acid
XX (PHCA). The method comprises converting cinamate to PHCA by converting
XX glucose to phenylalanine to PHCA through the phenyl ammonia-lyase (PAL)
XX route or by generating a new biocatalyst possessing enhanced tyrosine
XX ammonia-lyase (TAL) activity. The method is useful for the biological
XX production of PHCA which is useful as a monomer for the production of
XX Liquid Crystal Polymers (LCP), where the LCP is used in electronic
XX connectors, telecommunications and aerospace applications. LCP is also
XX useful in medical devices, as well as chemical, and food packing
XX applications due to its resistance to sterilising radiation. The present
XX sequence is Jerusalem artichoke (Helianthus tuberosus) cytochrome P-450
XX reductase enzyme DNA. Cytochrome P-450 and cytochrome P-450 reductase are
XX useful for the conversion of cinamate to PHCA
XX
XX Sequence 1863 BP; 531 A; 382 C; 424 G; 526 T; 0 U; 0 Other;
XX
XX Query Match 30.5%; Score 807.6; DB 6; Length 1863;
XX Best Local Similarity 67.2%; Pred. No. 4.2e-207;
XX Matches 1197; Conservative 0; Mismatches 559; Indels 24; Gaps 3;
XX
XX 415 TTGGCAGCAAGAAATTAGGCAAGTACCAAGACGAGTGTGTTAAAGTAGTTGACCTGGAT 474
XX 1 TTGTTTGAAGCGAAGCGCGATATGAAAGAGCTGTGTTTAAAGTGGTTGATTTGGAT 60
XX
XX 475 GACTATGACCGGAGATGATCAATATGAAGAGAAATTTAAAGAAAGAGTCTTTGGTGT 534
XX 61 GATTATGCTGCTGATGATGAGGATATGCAGAGAAATTCAGAGGAGACATTTGCTTIC 120
XX
XX 535 TTCAATGTTAGCCACTTATGATGATGTTAGTGGAGCCAACTGACAAATGCTGCGAGATTTTCAAA 594
XX 121 TTCTTCTTGGCTACATATGAGATGTTGAGCCAACTGATTAATGCTGCAAGATTTTATAAA 180
XX
XX 595 TGGTTCACTCAGGAACATGAAGGGAGAGTGGCTTCAGCAACTAACTATATGTTGTTTTT 654
```

QY 1720 ACTCAATTATCATGTTGGGACCTGGTACAGGGTTAGCTCTTTCAGAGGATTTCTGCAG 1779
DB |||||
QY 1312 GTCCCGGTATCATGATGTCCTCGGACCGGGTGTGCTCGTTAGAGGTTTCTTCAA 1371
DB |||||
QY 1780 GAAAGAAATGCGCCCTCAAGGAAATGGTGCTCAACTTGGCCCGCAGGTGCTCTTTTCGGA 1839
DB |||||
QY 1372 GAAAGATTAGCTCTCAAGGAATCTGGAACCGAACTCGGTCAATCCATTTTGTCTTCGGT 1431
DB |||||
QY 1840 TGTAGGAATGTAATATGGGACTTCAATTTATGAGACCAACTAACAACCTTCGTGGAACGA 1899
DB |||||
QY 1432 TGCAGAACCGTAAGTGGATTTTATATATGAGAACTGAACAACTTTGTGAAAT 1491
DB |||||
QY 1900 GGAATCAATTTCCGAGCTAGTTATTTCCCTTTTTCAGTGAAGGGAAGAAAGGAATATGTT 1959
DB |||||
QY 1492 GCGCGCTTTCCGAGCTTGACATGGCTTTCTCGGAAAGCGCATCTAAGATACGTG 1551
DB |||||
QY 1960 CAACATAAGATGATGGAAGAACCGGATGTATGGAATGTATATCAGGGGACGGTTAT 2019
DB |||||
QY 1552 CAACATAAATGAGCCAAAGGCTTCGATATATGGAACATGCTTTCTGAGGGAGCATAC 1611
DB |||||
QY 2020 CTCTATGTGTGATGATGCAAGGGAATGCGCAGAGATGTCATCGCAGTTGCATACC 2079
DB |||||
QY 1612 TTATACGTGTGTGATGCAAGGCTTCGCTAAGAGATGTACACCGAACCTTTCACACC 1671
DB |||||
QY 2080 ATTGCCCAAGAACAGGACCCATGGAATCATCTGCTGCCGAAGCTGCAGTAAAGAACTC 2139
DB |||||
QY 1672 ATTGTGCAAGAACAGGAAATTTGGATCTCTTAAGCAGAGCTGTATGTGAAGATCTA 1731
DB |||||
QY 2140 CAAGTTGAAGACGATATCTAAGAGATGTCTGTGATCGA 2179
DB |||||
QY 1732 CAAATGTCGGAAGATACCTCCGATGATTTTGTGTGATCTA 1771
DB |||||

RESULT 12

ADJ10845
ID ADJ10845 standard; DNA; 1985 BP.
XX
AC ADJ10845;
XX
AC ADJ10845;
XX
DT 17-JUN-2004 (first entry)
XX
DE Recombinant tomato DNA to generate disease resistant plants SeqID 241.
XX
KW genetically engineered; plant; Avr-Pto; avirulent Pto;
KW bacterial speck disease; tomato; transgenic; biotic; abiotic stress; ds;
KW Pfi.
XX
OS Lycopersicon esculentum.
XX
PN US2004006787-A1.
XX
PN 08-JAN-2004.
XX
PN 14-JAN-2003; 2003US-00341961.
XX
PN 14-JAN-2002; 2002US-0348792P.
PR 20-JUN-2002; 2002US-0390249P.
XX
XX (MART/) MARTIN G B.
PA (MYSO/) MYSOORE K K.
PA (CRAS/) CRASTA O R.
PA (FOLK/) FOLKERTS O.
PA (SWIR/) SWIRSKY P.
XX
XX Martin GB, Mysore KK, Crastra OR, Folkerts O, Swirsky P;
PI WPI; 2004-081759/08.
XX
XX New genetically engineered plant comprising a recombinant polynucleotide
PT showing expression associated with Avr-Pto mediated defense response,
PT useful in increasing resistance of plant against bacterial speck disease.
XX

PS Claim 5; SEQ ID NO 241; 176pp; English.

XX This invention relates to a method of generating novel genetically
CC engineered plants. Specifically, it refers to compositions useful for
CC transforming plants with a recombinant polynucleotide or plant gene that
CC shows a specific pattern of expression associated with the Avr-Pto
CC mediated defense response. Avr-Pto is described as the avirulent Pto gene
CC found in *Pseudomonas syringae* pathovar tomato strain [strain TI(A)],
CC which mediates bacterial speck disease in tomato plants. The present
CC invention describes identifying genes that are up- or down- regulated in
CC the defense response and that are involved in the interaction of Avr-Pto
CC with Pto and/or Pfi. As such, these novel recombinant polynucleotides
CC can be used to generate transgenic plants that are resistant to bacterial
CC speck disease and furthermore exhibit increased resistance against biotic
CC and abiotic stresses. This polynucleotide sequence is a recombinant
CC tomato polynucleotide used to generate genetically engineered, disease
XX resistant plants of the invention.

SQ Sequence 1985 BP; 538 A; 379 C; 464 G; 604 T; 0 U; 0 Other;

Query Match 29.1%; Score 770.2; DB 12; Length 1985;
Best Local Similarity 88.0%; Pred. No. 5.5e-197;

Matches 1126; Conservative 0; Mismatches 508; Indels 21; Gaps 3;

QY 542 TAGCCACTTATGTGTGATGGTGAGCCCAACTGACAACTGCGAGATTTTACAAATGGTTCA 601
DB |||||
QY 3 TGGCAACATATGAGATGTGTGAACCACTGATATATGTCGCAATTTCTATAATGGTTG 62
DB |||||
QY 602 CTCAGGAACATGAAGGGGAGAGTGGCTTTCAGCAACTTAATTTATGGTGTGTTGG 661
DB |||||
QY 63 AAGAGGGGAAAGAGAGGGGTGACTGCTTTAAGAACTCTTCAGTATGAGTATTTGGGCTG 122
DB |||||
QY 662 GTAACCGTCAATACGAGCATTTCAACAAGATCGGGTAGATGGGATGAGCACTCGGTA 721
DB |||||
QY 123 GCAACAGACAATACGAGCATTTTAAACAAGATGTCTAAAGTTGTCGATGAGCTTCGCTG 182
DB |||||
QY 722 AACAAAGTGCAGAAAGCGCATTTGTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATGAAG 781
DB |||||
QY 183 AGCAAGTGGGAGAGGCTTTGTTCCAGTGGGTCTTGGAGATGATGATCAATGCAATGAAG 242
DB |||||
QY 782 ATGATTTTACTGCTTGGCGAGAAATTTGTGGACTGAAATGGATCAGTTGCTCAAGATG 841
DB |||||
QY 243 ATGATTTTCTGTCATGGCGTGTAGTGTGGCTGAAATAGATAAGTTGCTTCTTGACG 302
DB |||||
QY 842 AGGATCTCTCTTTCAGTGGCTACACCGTATATTTGCTACTGTTCTGATACAGGCTAG 901
DB |||||
QY 303 GGGATGATGCAACT---GCTACAACCTCCATATACCTGCTGTTTGGGAATATAGGGTTG 359
DB |||||
QY 902 TGATTCACGAAACTACGGTCCGGCTCTCGATGATATAACACATAAA---TACTGCTAAACG 958
DB |||||
QY 360 TTACCTATGCAAGTCCAACTTTGATACGACTTGGACCAACAAATGTCATGCAATG 419
DB |||||
QY 959 GCGATGTGCATTTGATATTTCTCCATCTTTCAGAAACCAATGTTGCTCAACAAAGAGAGC 1018
DB |||||
QY 420 GACATGTCATCGTTGATGCTCAACATCTCTGTCAGAGCTAATGTTGCTGAGGAAGAGC 479
DB |||||
QY 1019 TCCAGAAACCCAGTCTGATAGATCTGTATACATCTGAGTTCGACATATCAGGCTCTT 1078
DB |||||
QY 480 TTCATACCTCCAGCTTCTGATCGTCTTTCGACATCATCTGGAGTTGACATTTCTTGCACG 539
DB |||||
QY 1079 CCCTTACATATGAGACTGGAGATCATGTTGGTGTGTTTATGCTGAGAACTGCGATGAAACTG 1138
DB |||||
QY 540 GACTTACGTACGAACTGGTGTATCATGTTGGTGTGTGTGCTGTGAAATTTTGTGAAACCG 599
DB |||||
QY 1139 TCGAGGAACAGGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCAATTTCAACCG 1198
DB |||||
QY 600 TGGAGGAAGCTGAAAGGCTACTGAATATATCACCGGATACTTTCTTTTCCATTACACCG 659
DB |||||
QY 1199 ATAAAGAACACGGGTCAACCCAGGAGCTCATTACCACCTCTTCCAGGCTCTTGA 1258
DB |||||
QY 660 ATAAAGAGGATGGCACACCACTTGGTGGAAAGTTCAATTTGCCATCTCCATCTCCCTCTTGA 719
DB |||||
QY 1259 CCTTACGATCTGCCCTAGCACGCTATGCTGATCTTTTGAATCCTCTCTAGAAAGGCTTCTC 1318
DB |||||

Db 720 CTTTGAGAACAGCATTGACTCGGTGCTGATGTTTGTAGTTCTCTCTAAAGTCTCTT 779
Qy 1319 TGAATGCTCTGTCGGCTATGCTATGACCCAGTGAAGCAGAGAGATTGCGCTTTTGT 1378
Db 780 TACTTGTCTTAGCGCATGTTCTTCGATCCAATGAAGCTGATCAATAGATATCTAG 839
Qy 1379 CATCACTCTGGGAAAGATGATATCAAAATGGGTAGTGGAAATCAGAGAGTCTTT 1438
Db 840 CATCACTCTGGGAAAGATGATATGCTCAGTGGATAGTTGCAAGTCAAGAGAGCTTC 899
Qy 1439 TGGAGATCATGGCGGATTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTCTGCGAG 1498
Db 900 TTGAAGTCATGGCTGAATTTCTTCAGCCAAAGCTTCAATCGGTGTTTCTTTGCTTCG 959
Qy 1499 TAGCCCTCTGCTTACCGCTCGATATCTATCTCATCTCTCTCTCTCTCTCTCTCT 1558
Db 960 TTGCTCTCGCTTACAACCAAGATTCTACTCCATCTCATCTCTCTCTCTCTCTCT 1019
Qy 1559 CAAGAATTCATGTAGCGTGTCTTTAGTATATGTTCAAGCCCTACCGGAAGGTTTACC 1618
Db 1020 CTAGAATTCATGTCACTGTGCACTGTGTTTACGACAAATGCCAAGTGGACGAATTCACA 1079
Qy 1619 GAGGAGTGTCTCGACATGATGAAGCATGCACTCTCTCAGG------TA 1663
Db 1080 AGGTTGTCTCTCAATGATGAAGATGCTATTCTCTAGAAAGAGCTTTCTCTGCA 1139
Qy 1664 GCTGGGCTCTATTTTGTTCGAACGTCAAACTTCAAGTTTACCAGTGCACCCCTCAACTC 1723
Db 1140 GTACGCGCACCTATTTTGTTCGCAATCAAACTTTAACTGCCAGCTGATATAAAGGTC 1199
Qy 1724 CAATTCATGTGGGACCTGTGTACAGGTTAGTCTCTTTCAGAGATTTCGACGAA 1783
Db 1200 CAATATAATGATGTGGCCCTGTACTGGAATGTCACCAATTCAGGGGTTTCTCCAGGAA 1259
Qy 1784 GAATGCCCTCAAGGAAATGTGTCTCACTTGGCCCGCAGTGTCTTTTTCGGATGA 1843
Db 1260 GAATGGCTTTGAAGGAGGAGGAGTGACCTTGGTCTCGAGTGTATTTTTGGATGCA 1319
Qy 1844 GGAATCGTATATGAGCTTCATTATTAAGACGCAACTTAAACAACTTCGTGGAACGAGGAG 1903
Db 1320 GGAACCGCAATGGACTACATCTATCAGGATGAGTTAGATAACTTCTTGAGCCGGTG 1379
Qy 1904 TCATTTGGAGCTAGTTATGCTTTTACGTGAAGGGGAAAGAGGAATATGTTCAAC 1963
Db 1380 CACTTTCTAATCTAGTTGTGCTTCTCAGTGAAGGACCTAACAAAGAAATATGTCAAC 1439
Qy 1964 ATAAGATGATGGGAAGCAACGGATGTATGGAATGTGATATCAGGGGACGTTATCTCT 2023
Db 1440 ATAAATGACACAAAGGCGGACACATCTGGAACATGATTTCTCAGGAGGTTATGTTT 1499
Qy 2024 ATGTGTGTGTGATGCCAAGGGAAATGGCCAGAGATGTCCATCGACGTTGCAATGATG 2083
Db 1500 ATGTGTGTGTGATGTAAGGGCATGGCCAGGATGTCCATCGGACCTTCACACTATTG 1559
Qy 2084 CCCAAGAACGAGACCCATGGAATCATCTGCTCCGAGCTGCAGTAAAGAACTCCAAG 2143
Db 1560 CTGAGGATCAGGATCATTGATAGCTTCCAAAGCCGAGAGCTTTGTGAAGAAATTTGCAAA 1619
Qy 2144 TTGAAGAACGATATCTTAAGAGATGTCTGGTGATCG 2178
Db 1620 CGACCGAGATATCTCGGTGATGTGTGTAATTG 1654

RESULT 13

ADA70621

ID ADA70621 standard; DNA; 2016 BP.

XX ADA70621;

AC ADA70621;

XX 20-NOV-2003 (first entry)

XX Rice gene, SEQ ID 3944.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
OS Oryza sativa.
XX WO2003000898-A1.
XX 03-JAN-2003.
XX 22-JUN-2001; 2001WO-IB001105.
XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX Claim 6; SEQ ID NO 3944; 899pp; English.
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC the expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2016 BP; 484 A; 464 C; 576 G; 487 T; 0 U; 5 Other;

Query Match 22.1%; Score 586.4; DB 8; Length 2016;
Best Local Similarity 60.7%; Pred. No. 2.5e-147;
Matches 1143; Conservative 1; Mismatches 577; Indels 161; Gaps 5;

Qy 319 AAAGAAGAGAGAGAGATTGAAGTTGATCTCTGTGTAATAATTAAGCTCACTATATTTTGGT 378
Db 271 AAGCAGGAGCGGAGCTTGACCCGACGACGAGGAGGTCGCCCTCTTCTTCGGC 330
Qy 379 ACTCAGACTGGTACTGCTGAAGATTGCTAAGGCATTTGGCAGAGAAATTAAGGCAAG 438
Db 331 ACGCAGACCGGACCGCCGAGGGCTTCGCCAAGGCGCTTCGGAGAGAGCCCAAGTCGAG 390
Qy 439 TACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACCGCAGAGATGATCAA 498
Db 391 TAGCAGAGCCCGCTCTTCAAGGTGCTGATCTGATGATGCTGCGGATGATGAGGAG 450
Qy 499 TATGAAGAGAAATTAAGAAGAGAGTCTTTGGTGTGTTTTCATGGTAGCCACTTATGTGAT 558
Db 451 TATGACAGAGCTTAAGAAGGAGATCATCGCCTTGTCTTCTGTCACACGCTATGGGAT 510
Qy 559 GGTGAGCCCACTGACATGCTCGGAGATTTTACAATGGTTTCACTCAGGAACTGAAGG 618
Db 511 GGGGAACCAACTGACAAATCGCGGAGGTTCTATAAATGGTTTGGAGAGGGGATGAGAGA 570
Qy 619 GGAGAGTGGCTTCAGCAACTTAACCTTATGGTGTGTTTGGTAAACCGTCAATACGAG 678
Db 571 GGTGATGTTGAGTAATCTTCGGTTTGGGTTCTTTGGCTCGGAAATAGGAGTACGAG 630
Qy 679 CATTTCAACAAGATCGCGGTAGATGATGAGTACGCAACTCGGTAAACAAGGTGCAAGCGC 738
Db 631 CATTTTAAACAGGTGGAAAGGTGGTTGACCAACTCTCTCGCTGAAACAAGGTGGAACGC 690

QY	739	ATTGTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATTGAAGATGATTTTACTGCTTGG	798
DB	691	ATTGTTCCCTCTTGCTTTTGGAGATGATGATCAATGCAATTGAGGATGACTTCAATGCAATGG	750
QY	799	CGAAGATTGTTGTGACATGAAATTCGATCAGTTGCTCAAGATGAGGATGCTGCTCCTTCA	858
DB	751	AAGGAACTTCTATGGCCAGAATTGGATTAATTTGCTCCGTGTTGAAGATGATAAATCGGCA	810
QY	859	GTGGCTACACCGTATATTGCTACTGTTTCTCGAATACAGGGTAGTGATTCACGAAACTACG	918
DB	811	GCACCAACTCCCTACACAGCTGCTATTCTCTGAATATAGAGTTGTTATGGTCAAGCCAGAG	870
QY	919	GTCCGGGCTGTGGATGATAAACAATAAATACTGCTAACCGCGAGTTGTGCATTTTGATATT	978
DB	871	GAAGCCATGCAATATCAACAAATCCCTTTAGTCTCAGTAATGGTCAATGCTATGCTATATGACATT	930
QY	979	CTCCATCCTTCAGAAACATTTGCTCAACAAGAGAGCTCCACAACCAACCAAGTCTGAT	1038
DB	931	CAGATCCTTCAGAGCAAAATGTGGCTGTGCGGGGGAGCTTTCACAGCCGGCTTCTTAC	990
QY	1039	AGATCTGTTATPACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATATGAGACTTGA	1098
DB	991	CGGTCTGCAATTTTAGAGTTTGAATTTTCAGGGACTGGTCTTACATATGAGACTTGA	1050
QY	1099	GATCATGTTGGTGTATTGCTGAGAACTGGGATGAATCTGTCGAGGA-AGCAGGGAGACT	1157
DB	1051	GATCATGTTGGTGTATATGCAGAAAACTGCACAGAGACTGTAGAGGAGAGTGTCTTTAATT	1110
QY	1158	GTTGGGTCAACCCCTGGATTTGCTGTTTTCAATTCACACGGATTAAGAAAGACGGGTCAAC	1217
DB	1111	GCCTTGGCTTCCCATGCACTGATCCCAAAGATGCTGAGAGGCTTAAGA-----	1158
QY	1218	CCAGGAAGACTCATTAACACCTCTTCCAGAGTCTTGCACCTTACGATCTGCCTTACG	1277
DB	1159	-----	1158
QY	1278	ACGCTATGCTGATCTTTTGAATCCTCTAGAAAGGCTTCTCTGATGCTCTGTCCGCTCA	1337
DB	1159	-----CATCTAGCATCTCTGCTGGAAAGTTTGTGGCTTCAACA	1195
QY	1338	TGCATCTGTACCCAGTGAAGCAGAGAGATTTGGCTTTTGTGATCATCCTCTGGGAAGAA	1397
DB	1196	TGAGCTTCA-----TTTGGCAGAA	1214
QY	1398	TGAGTATTCAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGCGCCAGATT	1457
DB	1215	GGAGTATTCTCAATGGATAGTTTCAAGTCAACGGAGTCTCTTGGAGTTATGACAGATT	1274
QY	1458	TCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTTGTGTCAGTAGTACCCCTCGCTTACCGCC	1517
DB	1275	CCCATCAGCAAAAGCCTCCACTTGGTGTCTTTTGGACCCATTTGCTCTCGAMTGCAGCC	1334
QY	1518	TCGNATCATTTCTATCTCATCC-----TCCTCTAAGTTTGTCTCCCTCAAGAATTCA	1568
DB	1335	GAGATACTACTCGATATCTCCCTTAACCGAGTKMCTTTGGATGACTCCAAACAAGAAATTC	1394
QY	1569	TGTGACGTGTCTTTAGTATATGTCACAAAGCCCTACCGGAAGGTTTACCGAGAGTGTG	1628
DB	1395	TGTAAATGTGCGCTAGTGTATGGCAAAACCCCTACTGTGAAGGATCCATAAAGAGATTG	1454
QY	1629	TTGCACATGGATGAAGCATCGAGTTCTCTCAGGA-----TAGCTGGGCTCC	1673
DB	1455	TTCTACTTGGATGAAGAACTCGATTCCCTTGGGAAGAGCCCAAGAATGTAGCTTGGGCTCC	1514
QY	1674	TATTTTGTGGAACGTCFAAATCTCAAGTTTACAGCTGACCCCTCAACTCCCAATTATCAT	1733
DB	1515	AATTTTGTGTAGGCAGTCFAAATCTCAAACTGCTTACTGATCTTACTGTGCTATTATAAT	1574
QY	1734	GGTGGGACCTGGTACAGGGTTAGTCTCTTTTACAGGGATTTCTGACGGAAGATGCGCCT	1793
DB	1575	GATAGGTCTCTGGAACTGGTCTTGACCTTTTAGGGGCTCTTACAGGAAGATTAAGTCTCT	1634
QY	1794	CAAGGAAAAATGGTGTCTCAACTTGGCCCCAGCAGTGTCTTTTTTTCGGATGTAGGAATCGTAA	1853

RESULT 14

REGISTRATION
ADR60759

ID ADR60759 standard; cDNA; 683 BP.

XX

AC ADR60759;

XX
XX
XX

DT 02-DEC-2004 (first entry)

XX

DE Cotton cDNA sequence, SEQ ID 1540.

XXII

Cotton; ss; plant; cold tolerance;

KW drought tolerance; plant disease r

KW plant growth regulator; heat toler-

homologous recombination; extreme

KW pathogen resistance; pest resistance

stress resistance.

XX QS *Gossypium hirsutum*

OS
XX
Gossypium hirsutum.

XX PN US2004181830-A1.

FN
XX
USZ004101030-A1.

PD 16-SEP-2004.

XX
17 OCT 1964
* 1400Z

29-JAN-2004; 2004US-00767795.

XX

PR 07-MAY-2001; 2001US-00849529.

PR 12-DEC-2001; 2001US-00021323.

XX
XX

PA (KOVA/) KOVALIC D K.

PA (ZHOU/) ZHOU Y.

PA (CAOY/) CAO Y.

THIS PAGE BLANK (USPTO)

db
449 ACGACGACGACGAGGTTGATGTTGCCGACGGGAAGACTAAGGTCACCTATTTTCTTCGGTA 508

; LENGTH: 2755									
; TYPE: DNA									
; ORGANISM: Glycine max									
; FEATURE:									
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140138C.1									
; US-10-424-599-44452									
Query Match 40.7%; Score 1079; DB 18; Length 2755;									
Best Local Similarity 74.6%; Pred. No. 5.9e-271;									
Matches 1404; Conservative 0; Mismatches 460; Indels 19; Gaps 3;									
Qy	311	TAATTGATAAAGAGAGAGAGATTGAAGTTGATCCTGGTAAATTAAGCTCACTATAT	370						
Db	446	TGAAGGAAGAAGAAGCAAGTCGATCGTCTGGTGGGAAGACCCGAGTTGCCATTT	505						
Qy	371	TTTTTGTTACTAGACTGTGCTGAGGATTGCTTAAGGATTGCGCAGGAAGAAATTA	430						
Db	506	TCTTCGGAATCAAACTGGTACCGCTGAGGGCTTTGCCAAGGCTTTGGCAGAGAGATCA	565						
Qy	431	AGCAAGATCAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGAGTACTATGCAGCCGAGG	490						
Db	566	AGCTAGGTATGAAGAAGCAGCTGTCAAGTTGCTGACCTGGATGACTATGCAATGAGTG	625						
Qy	491	ATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTGGTGTGTTTTTCATGGTAGCCACTT	550						
Db	626	ATGATCAATATGAAGAGAGAGCTGAAGAAAGAGTCACTTGCAATTTTCATGTTGGCAACAT	685						
Qy	551	ATGGTATGTGAGCCAACTGACAAATGCTGCGAGATTTTACAATGGTTCACTCAGG---	607						
Db	686	ATGGAGATGGAGGCCAACTGACAAATGCTGCAAGATTTCTACAAATGGTTTACTGAGGGTA	745						
Qy	608	AACATGAAAGGGAGAGTGGCTTCAAGCACTACTTATGGTGTGTTTTGGTTGGTAAACC	667						
Db	746	AAGCAGAGGGGTATCTGGCTTCA-CAGCTCAGTATGGTGTGTTTTGGCTTAGGTAACC	804						
Qy	668	GTCAATACAGAGCTTTCAACAAGATCGCGTAGATGTGGATGAGCAACTCGGTAAACAAG	727						
Db	805	GGCAATATGAACATTTTAAAGATAGTAAATAGTTGATGAAGAACTTAGTGAGCAAG	864						
Qy	728	GTGCAAGCCCATGTTTCAAGTGGGCTCGGTGACGATGATCAATGATGAAAGATGATT	787						
Db	865	GTGCAAGCCGCTTGTGTTCCATTGGGACTAGGTGATGACCATCAATCCATTTGAGGATGAT	924						
Qy	788	TTACTGCTGGCAGAGATTTCTGAGCTGAAATGGATCAGTTGCTCAAGATGAGGATG	847						
Db	925	TTGTTGCTTGAAGAGAACTCTATGGTCTGAGTTGATCAGTTGCTCCGGGATGAGGATG	984						
Qy	848	CTGCTCTCTCAGTGGGTACACCGCTATATTTGCTACTGTCTCTGAATACAGGGTAGTGATT	907						
Db	985	ATGTAATATCTGTATCTACTCTTATAAGGCTGCTATCTCTGAATATCGAGTTGTTATTC	1044						
Qy	908	ACGAAACTACGGTCGGGCTCTGATGATATAACACATATAATCTGTAACGGCGATGTTG	967						
Db	1045	ATGATTCACCGCTCACATCTTGCAATGATTAATCACTTAAATGGCAATGGTAAATGCTG	1104						
Qy	968	CATTGTATATCTCCATCTCTGAGTACCACTGCTTCTCAAAAGAGAGCTCCACAAC	1027						
Db	1105	TGTTGTATATTCACCATCTCTGAGGGTTAATATGCGGCTCAAGAGAACTTCAACAAC	1164						
Qy	1028	CCAAGTCTGATAGATCTGTATACATCTGGAGTTGACATATCAGGCTCTTCTCCTTACAT	1087						
Db	1165	CTGAGTCTGATCGTTCTTGATATACATTTGAGTTGACATATCCGGGACTGGCATATAT	1224						
Qy	1088	ATCAGACTGGAGATCATGTTGGTGTTPATGCTGAGAACTGCGATGAACTGTCGAGGAAG	1147						
Db	1225	ATGAAACTGGTGACCATGTGGGTGTTTTGCTGAAAACCGCGATGAACTGTTGAAAGAAG	1284						
Qy	1148	CAGGAGACTGTTGGGTCAACCCCTGGATTTGCTGTTTTTCAATTCACGGATAAAGAAG	1207						
Db	1285	CTGGAAGATTGCTGGGTGAGGATTTAGATTTGGTATTTTTCATTTCACACTAAATAGAG	1344						
Qy	1208	ACGGGTACCCCGGGAAGCTCATTTACCACTCTCTTTCCAGGCTCTTGCACTTACGAT	1267						

RESULT 3

US-10-425-115-98408
; Sequence 98408, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 98408
 ; LENGTH: 2892
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_21258C.1
 US-10-425-115-98408

Query Match 34.1%; Score 904; DB 20; Length 2892;
 Best Local Similarity 68.5%; Pred. No. 3.8e-225;
 Matches 1287; Conservative 0; Mismatches 570; Indels 21; Gaps 2;

QY	319	AAAGAAGAAGAGGAGATTGAAGTTGATCTCTGGTAAATAATTAAAGCTCACTATATTTTTGGT	378
DB	319	AAGGTGGACGCCGACGCGGAGCTTGATGACGCGCGGAAGCGCTCACCATCTCTTTCGGC	378
QY	379	ACTCAGACTGGTACTGCTGAAGATTGCTTAAGCAATTGGCACAAGAAATTAAGGCAAG	438
DB	379	ACACAGACTGGCACCCCGGAGGGTTTCGCAAGTCCATGGCGAGGAGCGAGGGCGCG	438
QY	439	TACAAGAAGACAGTTGTTAAAGTAGTTGACCTGGATGACTATGCAGCGCAGGAGTATCA	498
DB	439	TACGAGAGGCCGTGTTCAAAGTGGTGATCTGGATGACTATGCTCAGGAGGACGAGGA	498
QY	499	TATGAAGAGAAATTAAGAAGAGTCTTTGGTGTGTTTTCATGTTAGCCACTTATGGTAT	558
DB	499	TACGAGAGAAAGCTGAAGAAGGAACTGTGGTGTCTGTTCTCTAGCAAATATGGGAT	558
QY	559	GGTGACCAACTGACAACTGCTGGAGATTGTAACAATGGTTCACTCAGGAACATGAAGG	618
DB	559	GGGAGCCCACTGATTAATGAGCAGCACTGTAACAATGGTTTACTCAGGGAAGAGAA	618
QY	619	GGAGAGTGGCTTCAGCAACTAACTTATGGTGTGTTTGGTTGGTTAAACCGTCAATACGAG	678
DB	619	GAAGTTTGGCTGAAGGATCTTAATATGGTATTTTGGCTTGGAAACAGGCAATACGA	678
QY	679	CATTCAACAAGATCGGGTAGATGAGTAGAGCAACTCGGTAAACAAGGTGCAAGCGC	738
DB	679	CATTTTAAAGGTTGCAAGGTTGGTAGATGAGTAGTAGAGGAGCAGGTTGGGAAACGT	738
QY	739	ATTGTTCAAGTGGGCTCGGTGACGATGATCAATGCAATGCAATGATTTTACTGCTGG	798
DB	739	CTTGTTCCTGTTGGCTTGGAGACGATGATCAGTGCATTTGAGGATGATTTACTGCA	798
QY	799	CGAAGATTTGTTGGACTGAATTTGGATCAGTTCTCAAGAATGAGGATGCTGCTCTTCA	858
DB	799	AAGAATAGTGTGGCCAGAAATTAGATCAATGCTCTGGGACGAGATGACAACCTGGT	858
QY	859	GTGGCTACACCGTATATGCTACTGTTCTGTAATA CAGGGTAGTGAATTCACGAAACTACG	918
DB	859	GCATCGACTCCATATACTGCTGTAATCTCTGTAATACAGAGTTGTTTTCATTGCAAACT	918
QY	919	GTCCGGCTCTGGATGATAAACAATTAATCTGCTAAACGGGATGTTGCAATTTGATAT	978
DB	919	GACCTGTCAATCCAGATGATCATGGACACTAGCAACAGGTAAGGTTGATTTGATAT	978
QY	979	CTCCATCTTTGCAGAACCAATTTGCTCAACAAGAGAGCTCCACAACCCCAAGTCTGAT	1038
DB	979	CAACACCTTGCAGGCTTAATGTTGCTGTTCCGAAGAGCTGCACAAACGAGCTTCAGAT	1038
QY	1039	AGATCTGTATACATCTGGAGTTTGCATATACAGGCTCTTCCCTTACATATGAGACTGA	1098
DB	1039	CGCTCTTGTATCCATCTCGAGTTTGAATTTCTGGCACTGGTCTTGTGATGAACCGGA	1098

QY	1099	GATCATGTTGGTGTGTTTATGCTGAGACTCGGATGAACCTGTCGAGCAAGCAGGGAAGCTG	1158
DB	1099	GACCATGTTGGTGTATATGATCAGAAAATCTGTGTACACTGTGGAGAGGTGTGAAGGCTA	1158
QY	1159	TTGGGTCAACCCCTGATTTGCTTTTCAATTCACACGGATAAAGAAACGCGGTCACCCC	1218
DB	1159	CTTGACCTTTTCCAGACACATCTTCTCCATCCATGAGATGAGATGATGATCTCCT	1218
QY	1219	C-----AGGGAAGCTCATTAACAACCTCTTTCCAGGTCCTTTGCACTTACGATCTGCC	1272
DB	1219	CGTAAAGAGGAGGAGTTCTTTGGCCCCACCTTTCCATCTCCATGTACCTTGGGACTGCG	1278
QY	1273	CTAGCAGCTATGCTGATCTTTTGATCTCTCTAGAAAAGCTTCTCTGATTTGCTGTCTG	1332
DB	1279	CTTCTACGATATGCTGATCTACTCAATCCACGAAGAAGGCTGCTTTGCTTGTCTTAGCT	1338
QY	1333	GCTCATGCTATCTGTACCCAGTGAAGCAGAGAGATTGCGCTTTTGTGTCATCACCTCTGGGA	1392
DB	1339	TCTCAGCATCTGATCCAGCTGAAGCTGAGCACTTAGAATTTTGGCTTCTCTCTCTGGA	1398
QY	1393	AAGAAATGAGTATTTCAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCC	1452
DB	1399	AAGGATGAGTATTTCTCAATGAGTAACTGCTAGTCAGAGGAGCTTCTTGAAGTTATGGCC	1458
QY	1453	GAGTTTCCATCAGCAAAACCCCTCTTGTGTGTTCTTTGCTGCACTAGCCCTCGCTTA	1512
DB	1459	GCATTCCTTCTAGCTAAGCCACCACTGGGAGTGTTTTTCAGCAATAGCTCTCTCTCTG	1518
QY	1513	CGCCTCTGATATCTTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAATTTCAATGTG	1572
DB	1519	CAACCAGATATCTACTCAATTTTCATCATCTCCAAAGATGGCTCCCTCCAGAAATTCATGTA	1578
QY	1573	AGTGTGCTTTTAGTATATGGTCAAGCCCTACCGAAGGTTTACCGAGAGGTGTTCTCG	1632
DB	1579	ACATGTGCTTAGTTTATGGGCTTTCACCAACAGGAAGGATCCACCAAGAGGTTTGTTC	1638
QY	1633	ACATGGAATGAAGTCAAGTCTCTCAGG-----TAGCTGGGCTCTCTATT	1677
DB	1639	ACATGGAATGAAGTCAAGTCTCTCAGGAAATATAGCGAAGATGCGAGCTGGGCTCCATC	1698
QY	1678	TTTGTTCGAACCTCAAACTTCAAGTTTACCGAGCTGAGCCCTCAACTCCAATTTATCATGGTG	1737
DB	1699	TTTGTGAGCAGTCAAAATTTCAAGTTTACCTGCTGATCCCTCCACTCTTATTAATCATGAT	1758
QY	1738	GGACCTGTGTACAGGTTAGCTCTTTTCAAGAGATTTCTGCAAGAAAGATGCGCCCTCAAG	1797
DB	1759	GGTCTCTGGACAGGCTGCTCTTTTGAAGGCTTCTTGAAGGAGTTAGCATTTGAAA	1818
QY	1798	GAAATGGTGTCTCACTTGGCCGACGAGTGTCTTTTTCGGATGTAGGAATCGTATATG	1857
DB	1819	CAATCTGGGGCAGAAATTTGGGCACCTTCAATCTTTTCTTTTGGATGCGAGAACCGTAATG	1878
QY	1858	GACTTCATTTATGAAGACGAACCTAAACAACTTCGTGGAAACGAGGAGTCAATTTCCGAGCTA	1917
DB	1879	GACTACATATATGAAGATGAGTTGCAAACTTTCTTGGAGAGGGGCGCTTCTTGAGCTA	1938
QY	1918	GTTATGCTTTTTCAGTGAAGGGGAAAAGAGGAATATGTTTCAACATGAAGATGAGAG	1977
DB	1939	ATTGTTGCTTCTCTCGGAAGGGGCAACGAAGAATAATGTCAGCATAAAGATGGTGAA	1998
QY	1978	AAAGCAACGGATGATGGAATGATATCAGGGGACGGTTATCTCTATGTTGTTGGTGAT	2037
DB	1999	AAGGCCACAGATATTTGGAAACATCATCTCAAAATGGTGGTTACTTATATGTTTGGCGTGAT	2058
QY	2038	GCCAAAGGAATGGCCAGAGATGTCATCGCATCGTTCGATACCAATTTGCCCAAGAACAGGGA	2097
DB	2059	GCCAAAGGAATGGCTAGAGATGTACACAAAATGCTTCATACAAATAGTCCAAGAGCAGGGA	2118
QY	2098	CCCATGGAATCATCTGTGTCGGAAGCTGCAAGTAAAGAACTCCAAAGTTGAAGAACATAT	2157
DB	2119	TCTTTGGATAACTCTCAAAACCGAGAGCTATGTAAAGAGCTTGCAGATGGAAGGAAGGTAC	2178
QY	2158	CTAAGAGATGTCTGGTGA	2175

Qy	1591	CAAACTTCAAGTTACGAGCTGACCCCTCAACTCCAAATTATCATGGTGGGACCTGGTACAG	1750
Db	1652	CCAACTTCAAGACTTCTTCTGATTCTAAGGTACCGATCATCATCGTCCAGGGAAGT	1711
Qy	1751	GTTTAGCTCCCTTTTCAGAGGATTTCTGCAGGAAGAATGGCCCTCAAGGAAAAATGGTCTC	1810
Db	1712	GATTAGCTCCATTCAGAGGATTCCTTCAGGAAGACTAGCGTTGGTAGAATCTGGTGTG	1771
Qy	1811	AACTTGGCCGACGAGTGTCTCTTTTTCGGATGTAGGAATCGTAATATCGACTTCATTTATG	1870
Db	1772	AACTTGGCCCATCAGTTTGTCTTTGGATCGAGAAACCGTAGAATGGAATTCATCTACG	1831
Qy	1871	AAGACGAACTAAACAACTTCGTGAAACGAGGAGTCATTTCCGAGCTAGTTATTGCGCTTTT	1930
Db	1832	AGGAAGAGCTCCACGCAATTTGTTAGAGTGGTGTCTTCGCAGAGCTAAGTGTGCGCTTCT	1891
Qy	1931	CACGTGAAGGGGAAAAAGAGGAATATGTTCAACATAAGATGATGGAGAAAGCAACGGATG	1990
Db	1892	CTCGTGAAGNACCCACCAAGAAATACGTAACGACACAGATGATGGACAAGCTTCTGATA	1951
Qy	1991	TATGGAATGTGATATCAGGGGAACGGTTATCTCTATGTGTGTGTGATGCCAAGGGAATGG	2050
Db	1952	TCTGGAATATGATCTCTCAAGGAGCTTATTTATATGTTTGTGTGTGACGCCCAAGGCATGG	2011
Qy	2051	CCAGAGATGTCCATCGACGTTTGCATACCAATTGCCCAAGAACAGGGAACCCATGGAATCAT	2110
Db	2012	CAAGAGATGTTCACAGATCTCTCCACAATAGCTCAAGAACACGGGGTCAATGGATTCAA	2071
Qy	2111	CTGCTGCCGAAGCTGCAGTAAAGAAACTCCAAAGTTGAAGAACGATATCTAAGAGATGTCT	2170
Db	2072	CTAAGCAGAGGGCTTCGTGAAGNATCTGCACACGAGTGGAGNATCTTAGAGATGAT	2131
Qy	2171	GGTGA	2175
Db	2132	GGTAA	2136

RESULT 6

```

US-09-938-842A-803
; Sequence 803, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 803
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-803

```

Qy	266	AATCTTCGTCTTCTCAATCAAAACCTATTTGAAACTTATAAACCAATAAATTTGATAAAGAG	325
Db	221	GATCCGGTTCTGGGAAATTCAAAACGTCTCGAGCCTCTTAAGACCTTTGGTATTAAAGCCTC	280
Qy	326	AAGAGGAGATTGAAGTTGATCCTGGTAAAAATTAAAGCTCACTATATTTTTTGGTACTCAGA	385
Db	281	GTGAGGA--AGAGATTGATGATGGGCGTAAAGAAAGTTTACATCTTTTTTCGGTACACAAA	337
Qy	386	CTGGTACTGCTGAAGGATTTTGCTAAGGCATTTGGCAGAGAATAATTAAGCCAAAAGTACAAGA	445
Db	338	CTGGTACTGCTGAAGGTTTTCGAAAAGCTTTAGGAGAAGAAGCTAAAGCAAGATATGAA	397
Qy	446	AAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCGGAGGATGATCAATATGAAG	505
Db	398	AGACCAGATTCAAAATCGTTGATTGATTGATTAACGGCGCTGATGATGATGATGATGAGG	457
Qy	506	AGAAATTAAGAAGAGCTTTTGGTGTTTTTCATGTTAGCAGCTTATGTTGATGCTGAGC	565
Db	458	AGAAATTTGAAGAAGAGGATGTGGCTTCTCTTCTTAGCCACATATGGAGATGGTGAGC	517
Qy	566	CAACTGACAATGCTCGAGAGATTTTACAAATGGTTTCACTCAGGAACATGAAGGGGAGAGT	625
Db	518	CTACCGACAATGCAGCGAGATTCTACAAATGGTTTACCGAGGGGAATGACAGAGGAGAA	577
Qy	626	GGCTTCAGCAACTAACTTATTTGGTGTTTTTGGTTTGGTAAACCGTCAATACGAGCATTTCA	685
Db	578	GGCTTAAGAACTTGAAGTATGGAGTGTGTGGATTAGGAAACAGACAATATGAGCATTTTA	637
Qy	686	ACAAGATCGGGTAGATGTCGATGAGCAACTCGGTAAACAAGGTGCNAAGCGCATTTGTTTC	745
Db	638	ATAAGGTGTCGCAAGTTGTAGATGACATCTCTGTGCAACAAGGTGCACAGCTCTTTGTAC	697
Qy	746	AAGTGGGGCTCGGTGACGATGATCAATGCAATGCAAGATGATTTTACTGCTTGGCGAGAAT	805
Db	698	AAGTTGCTCTGGAGATGATGACGAGTGATTTGAGATGACTTTTACCGCTTGGGAGAG	757
Qy	806	TGTTGTGGAATGGAATGAGTTGAGTTGCTCAAGATGAGGATGCTGCTCTTCAAGTGCGCTA	865
Db	758	CATTGTGGCCGAGCTTGATACAAATCTGAGGGGAAGAAGGGGATACAGCT---GTTGCCA	814
Qy	866	CACGTTATATGCTATGTTTCTGTAATACAGGGTAGTGATTTACGAAACTACCGTCCGG	925
Db	815	CACATACACTGAGCTGTGTTAGAAATACAGAGTTTCTATTTCAGACTCTGGAAGATGCCA	874
Qy	926	CTCTGGATGATAAACACATAAACTGCTAAACGGCGATGTTGCAATTTGATATTCTCCATC	985
Db	875	ANTTCAATGATATAACATGGCAATGGGAATGGTTACACTGTGTTTGATGCTCAACATC	934
Qy	986	CTTGCAAGACCATTTGTTGCTCAACAAGAGAGCTCCACAAACCAGCTCTGATAGATCCT	1045
Db	935	CTTACAAAGCAATGTGCTGTTTAAAGGAGCTTTCATCTCCGAGTCTGATCGTTCTT	994
Qy	1046	GTATACATCTGGAGTTGACATATCAGGCTCTCCCTTTACATATGAGACTGGAGATCATG	1105
Db	995	GTATCCATTTTGGAAATTTGCAATTTGCTGGAAGTGGACTTACGTATGAACTGGAGATCATG	1054
Qy	1106	TTGGTGTATGCTGAGAACTGCGATGAACTCTGCGGAAGCAGGGAAGCTCTTGGGTC	1165
Db	1055	TTGGTGTACTTTGTGATAACTTAAGTGAACCTGTAGATGAAGCTCTTAGAATTTCTGGATA	1114
Qy	1166	AACCCCTGGATTTGCTGTTTTTCAATTTACACGGATAAAGAAGACGGGTCAACCCAGGAA	1225
Db	1115	TGTCACCTGATACTTTATTTCTCACTTACGCTGAAAAGAAGACGCACACCAATCAGCA	1174
Qy	1226	GCTCATTAACACCTCTTTTCCGAGGTCTTTGCACTTTACGATCTGCCCTAGACGCTATG	1285
Db	1175	GCTCACTGCTCTCCCTTCCCA---CCTTGTCAACTTGAGAACAGCGGCTTTACACGATATG	1231
Qy	1286	CTGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATTTGCTGCTCGGCTCATGCATCTG	1345
Db	1232	CATGCTCTTTTGAGTTCTTCAAAGAAGTCTGCTTTAGTTGGTTGGCTGTCTATGCATCTG	1291
Qy	1346	TACCCAGTGAAGCAGAGAGATTGCGGCTTTTTTGTCAATCCCTCTGGGAAGAAGATGAGTATT	1405

```
Db 1292 ATCTACCGAAGCAGAACGATTAACACCTGCTTCCACCTGCTGGAAAGGATGAATATT 1351
Qy 1406 CAAAATGGGTAGTTGGAAAGTCAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG 1465
Db 1352 CAAAGTGGGTAGTAGAGAGTCAAGAGTCTACTTGGAGTGTAGGCCGAGTTTCCCTCAG 1411
Qy 1466 CAAAACCCCTCTTGGTGTGTTCTTTGCTGAGTAGCCCTCGCTTACCGCCCTCGATACT 1525
Db 1412 CCAAGCCACACTTGGTGTCTTCTGCTGGAGTTGCTCCAAGGTGTCGAAGCTTAGGTCT 1471
Qy 1526 ATTCTATCTCATCTCTCCCTAAAGTTTGTCTCCCTCAAGATTCATGTGACGTGTCTTAG 1585
Db 1472 ATTCTGATATCATCATGCCCAAGATGCTGAACTAGAACTACGTACATGTGCACTGG 1531
Qy 1586 TATATGCTCAAGCCCTTACCGGAAGGTTTCCACGAGAGTGTGTTCACATGATGAAGC 1645
Db 1532 TTTATGAGAAATGCCAACTGGCAGGATTCTAAGGGAGTGTGTCCACTTGGATGAAGA 1591
Qy 1646 ATGAGTTCCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACGT 1690
Db 1592 ATGCTGTGCCCTTACGAGAAGTGAACACTGTTCTCGGCCGATATTTGTTAGGCAAT 1651
Qy 1691 CAAACTTCAAGTTACCAAGCTGACCCCTCAACTCCAATTATCATGTGGGACCTGGTACAG 1750
Db 1652 CCAACTTCAAGCTTCTTCTGATTTAAGTACCGATCATCATGATCGGTCCAGGACTG 1711
Qy 1751 GGTAGTCTCTTTTCCAGAGGATTTCTGCAGGAAAGATGGCCCTCAAGGAAATGGTGCTC 1810
Db 1712 GATTAGTCTCATTCAGAGGATTCCTTCAGGAAGACTAGCGTTGGTAGAATCTGGTTG 1771
Qy 1811 AACTTGGCCAGCAGTGTCTTTTTCGGATGTAGGAATCGTAATATGGAATCTCATTTATG 1870
Db 1772 AACTTGGGCCATCAGTTTGTCTTCTTGGATGCGAAGAACCCGTAGAATGGATTTTCATC 1831
Qy 1871 AAGACGAATCAACACTTCGTGCGACGAGGTCATTTTCGGAGCTAGTTATTTGCCCTTT 1930
Db 1832 AGAAGAGCTCCAGCGATTGTTGTAGAGTGGTGTCTTCGAGAGCTAAGTGTCCGCTTCT 1891
Qy 1931 CAGTGAAGGGGAAAAGAGGAATATGTTCAACATAGATGATGGAGAAACCAACGGATG 1990
Db 1892 CTCGTGAAGGACCACCAAGAAATACGTACAGCACAAGATGATGGACAAGCTTCTGATA 1951
Qy 1991 TATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTGATGCCAAGGGAATGG 2050
Db 1952 TCTGGATATGATCTCTCAAGGAGCTTATTTATATGTTGTGTGTGACGCCAAGGCAATGG 2011
Qy 2051 CCAGAGATGTCATCGCACGTTGCATACCATTCGCCAAGAACAGGGACCCATCGAATCAT 2110
Db 2012 CAAGAGATGTTACAGATCTCTCCACAAATAGCTCAAGAACAGGGGTCAATGGATTCAA 2071
Qy 2111 CTGCTCGGAAGCTGCAGTAAAGAACTCCAAGTTGAAGAACGATATCTAAGAGATGTCT 2170
Db 2072 CTAAGCAGAGGGCTTCGTGAAGATCTGCAACGAGTGTGAAGATATCTTAGAGATGTAT 2131
Qy 2171 GGTA 2175
Db 2132 GGTA 2136
```

RESULT 7

```
US-11-069-633-13
; Sequence 13, Application US/11069633
; Publication No. US20050208643A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt-Dannert, Claudia
; APPLICANT: Watts, Kevin
; TITLE OF INVENTION: Flavonoids
; FILE REFERENCE: 09531-160001
; CURRENT APPLICATION NUMBER: US/11/069,633
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: US 60/549,077
; PRIOR FILING DATE: 2004-03-01
```

```
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-069-633-13
```

```
Query Match 33.8%; Score 895.4; DB 24; Length 2136;
Best Local Similarity 67.3%; Pred. No. 5.6e-223;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;
```

```
Qy 206 TCATATATGTCACAACCTGTAGCTTCAATGCTGATTCGGATTTGGTTCTTCGATGTATGA 265
Db 161 TGATTTGTTACCACTTCCATTTGCTGTTCTTATTGGTTGTCATGCTTATGCTGTTGAGGA 220
Qy 266 AATCTTCGCTCTTCAATCAAAACCTTATTGAAACTTATAACCAATAAATTGATAAAGAAG 325
Db 221 GATCCGGTTCTGGGAATTCAAAACGTCGAGCCCTTTAAGCCTTTGGTTATTNAAGCCTC 280
Qy 326 AAGAGAGATTGAAGTTGATCCTGTGTAATAAATAAGCTCACTATATATTTTGGTACTCAGA 385
Db 281 GTGAGGA---AGAGATTGATGATGGCGTAAGAAAGTTTACCATCTTTTCGGTACACAA 337
Qy 386 CTGGTACTCTGAAGATTGCTTAAGGCATTGGCAGAAAGAAATTAGGCAAGTACAAGA 445
Db 338 CTGGTACTCTGAAGTTTTCAAAAGCTTTTAGGAAGAAAGCTAAAGCAAGATATGAA 397
Qy 446 AAGCAGTTGTTAAAGTGTGATGACCTGATGACTATGACGCGAGGATGATCAATATGAAG 505
Db 398 AGACCAAGATTCAAAATCGTTGATTGGATGATTAACGGCTGATGATGATGATGAGG 457
Qy 506 AGAAATTAAGAAAGAGTCTTTTGGTGTGTTTTCATGGTAGCCACTTATGTGATGTTGAGC 565
Db 458 AGAAATTAAGAAAGAGGATGTGGCTTCTTCTTCTTAGCCACATATGAGATGTTGAGC 517
Qy 566 CAACTGACAAATGCTGGAGATTTTACAAATGTTTCACTCAGGNAACATGAAGGGAGAGT 625
Db 518 CTACCGACAAATGCAGCAGATTTCTACAAATGGTTTCCAGGGGAAATGACAGAGGAAAT 577
Qy 626 GGCTTCAGCAACTAACTTATGTTGTTTGGTAAACCGTCAATACGACGATTTCA 685
Db 578 GGTCTAAGAACTTGAAGTATGGAGTGTGTTGGATTAGGAACACAGACATATGACATTTTA 637
Qy 686 ACAAGATCCGGTGTAGATGTGATGACAACTCGGTAAACAAGGTGCAAGCGCATTTGTC 745
Db 638 ATAAGGTTGCCAAAGTTGTAGATGACATTTCTGTCGAACAAGGTGCACAGCGCTTTGTAC 697
Qy 746 AAGTGGGCTCGGTGACGATGATCAATGCAATTCMAAGATGATTTTACTGCTTGGCGAGAAT 805
Db 698 AAGTTGGTCTTGGAGATGATGACCAAGTGTATTGAAGATGACTTTACCGCTTGGCGAGAAG 757
Qy 806 TGTGTGGAAGTCAATTTGGATCAGTTGCTCAAAAGATGAGGATGCTGCTTTCAGTGGCTA 865
Db 758 CATTTGGTGGCCGAGCTTGTATACAACTACGAGGAAGAGGGATACAGCT---GTGGCCA 814
Qy 866 CACCGTATATGCTACTGTTCTCGAATAACAGGGTAGTGTATTCAGAAACTACGTCGCGG 925
Db 815 CACCATACACTGCAGCTGTGTTAGATAACAGAGTTTCTATCACGACTCTGAAGATGCCA 874
Qy 926 CTCTGGATGATAAACAACATAAATACCTGCTAACCGGATGTTGATTTGATATTTCTCCATC 985
Db 875 AATTCAATGATATAAACATGCGCAATATGGGAATGGTTACACTGTGTTGATGCTCAACATC 934
Qy 986 CTTTGCAAGAACCAATTTGTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGTAGATCCT 1045
Db 935 CTTACAAAGCAAAATGTCGCTGTATAAAGGGAGCTTCACTACTCCCGAGTCTGATCGTTCTT 994
Qy 1046 GTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
Db 995 GTATCCATTTGGAATTTGCAATTTGCTGGAAGTGGACTTACGTATGAAACTGGGAGATCATG 1054
Qy 1106 TTGGTGTTTTATGCTGAGAACTGCGATGAAACTGTTCGAGGAAGCAGGGAAGCTGTTGGTGC 1165
```


Db 1218 GGGGAAGCGCCTTGTGCCAGTGGGTCTAGGTGATGATGATCAATGCAITTAGGATGACT 1277
Qy 788 TTAAGTCTTCGGCAGAAATCTTGTGGACTGAATTTGGATCAGTTGCTCAAGATGAGATG 847
Db 1278 TTAAGTCTTCGGCAGAAATCTTGTGGACTGAATTTGGATCAGTTGCTCAAGATGAGATG 1337
Qy 848 CTGCTCCTTCAGTGGCTACACCGGTATATCTGCTGCTGAATACAGGGTGTAGTTC 907
Db 1338 ATGCAACT--GTGCTACACCTTATCTGCTGAGTGGAGTACCGGGTGTATTC 1394
Qy 908 ACGAAATACGGCTCGCGGCTCTCGATGATGATAAACAATAATCTGCTAAACGGCGATGTTG 967
Db 1395 ATGATCCATTGGAAGCATCTGTGCGACGAAAGAAAGTGGCAATAATGTAATGGTTCAGGCCA 1454
Qy 968 CATTGTGATATCTCCATCTTCGAGAACCAATCTGCTCAACAAAGAGAGCTCCACAAAC 1027
Db 1455 TTGTGGATGCTCAACATCCAGTCAAGGCAATGTGGCTGTGAAAGGAGCTTCATACCTC 1514
Qy 1028 CCAAGTCTGATAGATCCTGTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACAT 1087
Db 1515 CTGCATCTGATGATCTTGCATCAITTTGGAATTTGACATTTTCAGGCATGGAGTTACAT 1574
Qy 1088 ATGAGACTGAGATCATGTTGGTGTATCTGCTGAGAACTCGGATGAAACTGTGCGAGGAG 1147
Db 1575 ATGAAACTGGGGACCATGTTGGTGTATCTGCTGAGAAATTTGTCTGAAACTGTGGAAGAGG 1634
Qy 1148 CAGGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCCAAATTCACAGGATAAAGAG 1207
Db 1635 CAATAGGTTAATAGGTTTGTCCACGATACCTATTTCTCAATCCATACCTGATGATGAAG 1694
Qy 1208 ACGGGTCAACCCAGGGAAGCTCAATACCACTCCTCTTCCAGGCTCTTGACACCTTACGAT 1267
Db 1695 ATGCAAAACCACTAGCGGAAGCTCCTTGCCACTACATTTCCACCCCTGTACTTAAGAA 1754
Qy 1268 CTGCGCTAGCAGTATGCTGATCTTTTGAATCCTCTGAGAAAGGCTTCTCTGATGCTC 1327
Db 1755 CAGCACTTGACGATATGCAAGATGTTTGAAGTTTCAACCCAAAAGTCTGCGCTTGGCT 1814
Qy 1328 TGTCCGCTCATGATCTGTACCCAGTGAACGACAGAGATTTGCG-CTTTTGTCTATCACCT 1386
Db 1815 TAGCTGCTCATGATCTGATCCATCTGAAGCTGATGACTTAAGACATCTTGGCTCACCT 1874
Qy 1387 CTGGGAAGATGAGTATTCAAATGGGTAGTTTGGAGTCAAGAGAGTCTTTTGGAGATC 1446
Db 1875 GCTGGAAAGGATGAATATTCAGAGTGGTGTATTTGCCTCTCAGAGAGTCTCCTTGAGTC 1934
Qy 1447 ATGGCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTCTTTTGTGTCAGTACGAGCCCT 1506
Db 1935 ATGGCTGAATTTCCATCAGCAAAACCTCCAAATTTGGTGTCTTTTTCAGCAGTGTGCTCCT 1994
Qy 1507 CGCTTACCGCTCGATACCTATCTATCTCATCTCTCCTCAAGTTTGTCTCCCTCAAGATT 1566
Db 1995 CGCTTGAGCTAGATTTTATTCATCTCTCATCTCCAAAGATGGTGCCAAACAGAAAT 2054
Qy 1567 CATGTGACGTGTGCTTTAGTATATGTTCAAGCCCTACCGGAAGGTTTCAACGAGAGTG 1626
Db 2055 CATGTTACCTGTGATAGTACATGAGAAATGCCCAACCGAAGGATTCACAAAGAGTG 2114
Qy 1627 TGTTGCAATGAGATGAGCATGAGTTCTCAGAA-----TAGCTGGCT 1671
Db 2115 TGTTCAACATGGATGAAGATTTCTGACCATTTGGAGAAAAGCCAGGATGCAAGTTGGCT 2174
Qy 1672 CCTATTTTGTGGAAGTCAAGCTCAAGTTACGAGTACCCCTCAACTCCAAATATC 1731
Db 2175 CCTATTTTGTGAGGACCTCAACTTTAGACTCCCTTCTGATTAATGAAGTGCCTATAATC 2234
Qy 1732 ATGGTGGGACCTGGTACAGGTTAGCTCCTTTTCAGAGGATTTCTGCGAAGAAAGATGGCC 1791
Db 2235 ATGATTTGCTCCTGGCACTGATGGTCTCTTTTCAGAGGTTTCTTTCAGGAAAGATTAGCT 2294
Qy 1792 CTCAAGAAATGGTGTCAACTTTGGCCAGCAGTGTCTTTTTCGATGTAGGAATCGT 1851
Db 2295 CTGAAGAGGAGGAGCTGAATCTGGCCCTCTCAGTTTATTTCTTTTGTGATGCAAGAACCTG 2354

Qy 1852 AATATCGACTTCATTTTATGAAGACGAATAACAACCTTCGTGGAACGAGGAGTCATTTGC 1911
Db 2355 CAAATGGACTACATCTATGAAGACGAGTTGATGTCATTTCTGTTATCTGGCGACTTGAT 2414
Qy 1912 GAGCTAGTTTATTCCTCTTTTTCAGTGAAGGGGAAAGAAATATGTTCAACATAAGATG 1971
Db 2415 GAGCTCATTTCTTGGCTTCTCTCGAGAGGGACCCACCAGGAGTATGTACAAACATAAAATG 2474
Qy 1972 ATGGAGAAAGCAACGGATGTATGGAATGTATATCAGGGGACGGTTATCTCTATGTGTGT 2031
Db 2475 ATGGAGAAAGCTTCAGAAATTTTGGAGCATGATATCAAGAGGAGCTTACATTTATGTGTGT 2534
Qy 2032 GGTGATGTCGAAGGAAATGCGCAGAGATGTCCATCGCACGTTCGCATACCATTTGCCCAAGAA 2091
Db 2535 GGTGATGCCAAGGCAATGCGCAGGATGTACACCGGCCCTGCACACAATTTTTCGAAGAG 2594
Qy 2092 CAGGGACCATGGAATCATCTGCTGCCGAAGCTGCAAGTGAAGAACTCCAAGTTGAAGAA 2151
Db 2595 CAGGGTTCTCTCGATAGTTTCCAAGGCTGAGAGCATGTTAAAGAACTTACAAACTACTGGC 2654
Qy 2152 CGATATCTAAGAGATGCTCTGGTGATCGAATGT 2183
Db 2655 AGATATTTCCGCGATGTATGGTGATGATATCT 2686

RESULT 10

US-10-429-949-18
; Sequence 18, Application US/10429949
; Publication No. US20040002105A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: ACHNINE, LAHOUCINE
; APPLICANT: SUZUKI, HIDEYUKI
; APPLICANT: HE, XIAN-ZHI
; APPLICANT: WANG, LIANGJIANG
; TITLE OF INVENTION: METHODS OF IDENTIFYING GENES FOR THE MANIPULATION OF
; FILE OF INVENTION: TRITERPENE SAPONINS
; FILE REFERENCE: NBLE002US
; CURRENT APPLICATION NUMBER: US/10/429,949
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/380,159
; PRIOR FILING DATE: 2002-05-04
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2581
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-429-949-18

Query Match 32.0%; Score 849; DB 17; Length 2581;
Best Local Similarity 65.3%; Pred. No. 8.7e-211;
Matches 1299; Conservative 2; Mismatches 667; Indels 21; Gaps 3;

Qy 203 TTTTCATTTATGTCACAACTGTAGCTTCAATGCTGATTCGATTTGCTTCTTCGCAATGTA 262
Db 228 TTATGATCTTAACAACCTTCAATAGCTGTTCTCATCGGTTGCGTCTGTTTAAATTTGGC 287
Qy 263 TGAATCTTTCGCTCTTCTCAATCAAAACCTTATGAAACTTATAAACCAATAATTGATAAAG 322
Db 288 GTAGATCCAAATCTTCAAAAACCAAAACCAATTTGAAGTTCCTAAACCGGTTATTCGAGA--- 344
Qy 323 AAGAAGAGGAGATTTGAAGTTGATCTCTGGTAAATTAAGCTCACTATATTTTTTGGTACTC 382
Db 345 AACTTCTTGAACCTTGAATCGATGACGGTACCAAAAAAGTTACCGGTTTCTTTTGGCAGTC 404
Qy 383 AGACTGGTACTGCTGAAGGATTTGCTAAGGCAATTTGCGAGAGAAATTAAGGCAAGTACA 442
Db 405 AAACCGGTACCGCGAAGGTTTTCGCAAGGCGATAGCGGAAGAGGCAAAAGCGCGTTATG 464


```

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1764)
; OTHER INFORMATION:
US-10-188-523B-13

Query Match      30.5%; Score 807.6; DB 16; Length 1863;
Best Local Similarity 67.2%; Pred. No. 4.9e-200;
Matches 1197; Conservative 0; Mismatches 559; Indels 24; Gaps 3;

QY 415 TTGGCAGAGAAATTAAGGCAAGTACAGAAAGCAGTTGTTAAAGTAGTTGACCTGGAT 474
DB 1 TTGTTTGAAGACGGAAGCGCGATATGAAGAAGCTGTGTTTAAAGTGGTTGATTTGGAT 60
QY 475 GACTATGACGCGAGGATGATCAATATGAAGAGAAATTAAGAGAAAGAGTCTTTTGGTGT 534
DB 61 GATTATGCTGCTGATGATGAGGAGTATGACAGAGAAATTCAGAAGAGAGACATTTGCTTTC 120
QY 535 TTCAATGGTAGCCACTTATGTTGATGTTGAGCAAGTACGCAATGCTCGGAGATTTTACAA 594
DB 121 TTCTTCTTGCTACATATGAGATGTTGAGCCTCAACTGATATGCTGCAAGATTTTATAAA 180
QY 595 TGCTTCACTCAGGAACAATGAAGGGGAGAGTGGCTTCAGCAACTAACTTATGTTGTTTTT 654
DB 181 TGCTTCAACCGAGGAGATGATAAGAGATTGCTTGAAGAACTTCACTATGTTGTTT 240
QY 655 GGTTCGGTTAACCGTCAATACGAGCAATTCACAAGATCGCGGTAGATGTGGATGAGCAA 714
DB 241 GGTCTTTGGCAACAACAGATGAGCATTTTCAACAGATTGCAATTAGTGGTTGATGAGGT 300
QY 715 CTCGGTAAACAAGGTGCNAAGCGCATTTTCAAGTGGGCTCGGTACAGATGATCAATGC 774
DB 301 CTCACAGAGCAGGTGCAAGCGCTTTGTTCCAGTTTGGCCTTGAGATGACGATCAATCA 360
QY 775 ATTGAAGATGATTTTACTGCTTCCGAGAAATTTGTTGGACTCAATTTGATGATGTTGCTC 834
DB 361 ATTGAAGATGATTTTCTGATGGAAGAAATTAAGTGTGGCTGATTTGATGATTTGCTT 420
QY 835 AAAGATGAGGATGCTGCTTCAAGTGGCTACACCGTATATTTGCTACTGTTCTCGAATAC 894
DB 421 CTTGATGAGACGACAAAGACT--GCTGCCACTCTTACACAGCTGCCATTCGCGAATAC 477
QY 895 AGGTTAGTATTCACGAATCAAGTCCGGCTCTGGATGATTAACACATTAATCTGCT 954
DB 478 CGAGTCTGTTTTCATGACAACTGATACGCTTTTCCGAGAACTCA-----TAGTCAAACT 531
QY 955 AACGGGATGTTGCAATTTGATATTTCTCCATCTTCCAGAACCAATTTGTTGCTCAACAAGA 1014
DB 532 AATGGTCACTACTGTTCAAGATGCTCAACATCCATGCGATCCAAACGTGGCTGTTAAAAA 591
QY 1015 GAGCTCACAAACCCAGTCTGATAGATCTCTGATATACATCTGAGATTCGACATATCAGGC 1074
DB 592 GAGCTCCATACCCCTGAATCCGATCGCTCTGCACTCATCTTGAATTTGACATCTCTCAC 651
QY 1075 TCTTCCCTTACATATGAGCTGAGATCATGTTGGTGTGTTATGCTCAGAACTCGGATGA 1134
DB 652 ACTGGAATATCATACGAAATCGGGATCAGTCCGGTGTCTACTGTGAAACCTTAATTGAA 711
QY 1135 ACTGTCGAGGAACGAGGAGCTGTTGGGTCAACCCCTGGATTGCTGTTTCAATTCAC 1194
DB 712 GTAGTGGAGGAAGCTGAGAACTGATAGGATTAACAGAGATACATTATTTCTCATTTACAC 771
QY 1195 ACGGATAAAGAACGGGTCAACCCAGGAGAGCTCAATTCACCTCTCTTCCAGGTCTT 1254
DB 772 ATTGATAAACGAAGATGAAACCACTCGGTGGACCTACATTTGAGCTCTCTTCCCTCC 831
QY 1255 TGCACTTACGATCTGCCCTAGCACGCTATGCTGATCTTTTGAATCCTCTAGAAAGGCT 1314
DB 832 TGCACTTTTAAAGAAAGATGAAACAAATACGAGATCTGTGAGTGTCTCCCAAAAGTCA 891
QY 1315 TCTCTGATTTGCTGTGCTCGCTCATGCTATGCTATGCTATGCTGAGGAGATGCGCTTT 1374
DB 892 ACCTTGCTGCTCTAGCTGCGCATGCTTCTGATGCCACTGAAGCTGATCGACTACAATTT 951
```

```

QY 1375 TTGTCAATCACCTCTGGAAAGAAATAGTATTCAAAATGGGTAGTTGGAAAGTCAGAGAGT 1434
DB 952 CTTGCAATCTCGTGAGGGCAAGGATGAATATGCTGAATGATTGTTGCCAAACCAAGAAGC 1011
QY 1435 CTTTGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGCT 1494
DB 1012 CTTCTTGAGGTATGGAAGCTTTTCGTCAGCTAAACCTCCGCTCGGGGTTTCTTTGCA 1071
QY 1495 GCAGTAGCCCTCGCTTACCGCTCGATACTATTCTATCTCATCTCTCTCTAAGTTTGTCT 1554
DB 1072 GCTATGGCCCGGTTTGAGCTCGATCTACTCTATTCTTCTCTCCCAAGATGGTA 1131
QY 1555 CCCTCAAGAAATTCATGTGACGTGTCTTTAGTATATGTTCAAAAGCCCTACCGGAAGGTT 1614
DB 1132 CCCAACAGGATTCATGTTACGTGTGCTTATGATGTTTATGAGAAGACTCTCGAGGTCGTATC 1191
QY 1615 CACCGAGGAGTGTGTCGACATGGATGAAGCATGCAATGTTCCCT-----CAG 1659
DB 1192 CACAAAGGAATATGCTCAACCTGGATGAAGAATGCTGTGCTTTGACCGAAATCAAGAT 1251
QY 1660 GATAGCTGGGCTCCTATTATTTTGTTCGAACGTCAAACTTCAAGTTACCAGCTGACCCCTCA 1719
DB 1252 TGCAGCTCGGACCCATTTTGTGTAGAACATCGAATCTCAGACTTCAGCTGACCTTAA 1311
QY 1720 ACTCAATTTATCATGTGTGGACCTGTGACAGGTTAGCTTCTTTCAGAGATTTCTGCGAG 1779
DB 1312 GTCCCGGTTATCATGATTTGGCCCTGGAACCGGCTGGCTCCGTTTAGAGGTTTCTTCAA 1371
QY 1780 GAAAGNATCGCCCTCAAGGAAATGTTGCTCAACTTGGCCCGCAGCTGCTCTTTTCGGA 1839
DB 1372 GAAAGATTAGCTCTCAAGGAATCTGGAACCGAATCTCGGTCAATTTGTTTCTTCGGT 1431
QY 1840 TGTAGGAATCTGAATATGGAATTTTATGAAGACGAATCAAACTTTCGTGGAACGA 1899
DB 1432 TGCAGAAACCGTAAAGTGGATTTTATATGATGAGATGAATCTGAACATTTGTTGAAAT 1491
QY 1900 GGAGTCATTTTCGGAGCTAGTTATGCTTTTTCAGTGAAGGGGAAAGAGATATGTT 1959
DB 1492 GCGCGCTTTCCGAGCTTGACATGGCTTCTCTCGCAAGCGGCATCTAAAGAATACGTG 1551
QY 1960 CAACATAAGATCATGAGAGAAACCAACGATGATGGAATGTGATATCAGGGGACGTTAT 2019
DB 1552 CAACATAAATGAGCCAAAGGCTTCGATATATGGAACATGCTTCTCAGGGAGCATAC 1611
QY 2020 CTCTATGTGTGTGATGCCAAGGAATGGCCAGAGATGTCCATCCGACGTTGCAATACC 2079
DB 1612 TTATACGTGTGTGATGCCAAGGATGGCTAAAGATGTACACGGAACCTTTCACACC 1671
QY 2080 ATTGCCAAGAACAGGGACCCATGGAATCATCTGCTGCCAAGCTGCAGTAAGAAGTCT 2139
DB 1672 ATTGTGCAAGAACAGGGAAATTTGGATTCCTCTAAAGCAGAGCTGATGTGAAGATCTA 1731
QY 2140 CAAAGTTGAAGAACGATATCTAAGAGATGCTGCTGATGCA 2179
DB 1732 CAAATGTCGGGAAGATACCTCCGTGATTTGGTGATCTA 1771
```

RESULT 13
US-10-341-961A-241
; Sequence 241, Application US/10341961A
; Publication No. US20040006787A1
; GENERAL INFORMATION:
; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.
; APPLICANT: Curagen Corporation
; APPLICANT: Crasta, Oswald
; APPLICANT: Swirsky, Peter
; APPLICANT: Mysore, Kiran
; APPLICANT: Folkerts, Otto
; APPLICANT: Martin, Gregory
; APPLICANT: Ekengren, Sophia
; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE
; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE

FILE REFERENCES: BTI.67A2
CURRENT APPLICATION NUMBER: US/10/341.961A
CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: 60390249
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 60261029
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60348792
PRIOR FILING DATE: 2002-01-14
NUMBER OF SEQ ID NOS: 395
SOFTWARE: Patencin version 3.1
SEQ ID NO 241
LENGTH: 1985
TYPE: DNA
ORGANISM: Lycopersicon esculentum
US-10-341-961A-241

Query Match 29.1%; Score 770.2; DB 17; Length 1985;
Best Local Similarity 68.0%; Pred. No. 3.1e-190;
Matches 1126; Conservative 0; Mismatches 508; Indels 21; Gaps 3;

QY	542	TAGCCACTTATGCTGATGGTGGAGCCCACTGACACATGCTGGAGATTTTACAAATGTTCA	601
DB	3	TGGCAACATATGAGATGGTGAACCACTGATAATGCTGCCGATTTCTATAAATGTTTG	62
QY	602	CTCAGGAACATGAAGGGGAGAGTGGCTTCAGCAACTAACTTATGGTGTGTTTGGTTGG	661
DB	63	AAGAGGGGAAGAGAGGGTGACTGCTTAAAGATCTTCAGTAAAGATTTTGGGCTTG	122
QY	662	GTAAACCGTCAATACGAGCACTTCAACAAGATCGCGTAGATGGATGAGCAACTCGGTA	721
DB	123	GCAACAGACAATACGAGCACTTAAACAAGATTCCTAAAGTTGTCGATGAGCTTCTGCTG	182
QY	722	AACAAGGTGCAAGCGCATTTGTTCAAGTGGGGCTCGTGACGATGATCAATGCAATGAAG	781
DB	183	AGCAAGGTGGCGAGAGGCTTGTTCAGTGGGCTTGGAGATGATGATCAATGCAATGAAG	242
QY	782	ATGATTTTACTGCTGGCGAGAAATGTTGTGGACTGAATTTGGATCAGTTGCTCAAAAGATG	841
DB	243	ATGATTTTGTGATGGCGTGGAGTGTGTTGAGTGTGAGTGTGATGATGATGATGATGATG	302
QY	842	AGGATGCTGCTCTCAGTGGGTACACCGTATATGCTACTGTTCTGTAATACAGGGTAG	901
DB	303	GGGATGATGCAACT--GCTACAACTCCATATACTGCTGCTGTTTGGGAATATAGGGTTG	359
QY	902	TGATTACGNAACTACGGTGGCGCTCTGGATGATTAACACATAAA--TACTGCTAAGC	958
DB	360	TTACCTATGACAAAGTCCAACTTTGATTAACGACTTGAACCAACAAATGGTCAATGCAATG	419
QY	959	GGCATGTTGCAATTTGATATTTCTCCATCTTGCAGAACCAATGTTGCTCAACAAAGAGAGC	1018
DB	420	GACATGTCATGTTGATGCTCAACATCTCTGTCAGAGTATGTTGCTGTGGAGGAGAGC	479
QY	1019	TCACAAACCCAAAGTCTGATAGATCTCTGTATACATCTGGAGTTGCGACATATCAGGCTCTT	1078
DB	480	TTCACTACTCCAGCTTCTGATCGTTCTTGCACTCATCTGGAGTTTGACATTTCTTGCACTG	539
QY	1079	CCCTTACATATGAGATGAGATGATGTTGGTGTGTTATGCTGAGAACTCGGATGAACTG	1138
DB	540	GACTTACGTACGAAACTGGGTGATCATGTTGGTGTGACTGTGAAATTTTGTGAAACCG	599
QY	1139	TCGAGGAAGCAGGGAAGCTGTGGGTCAACCCCTGGATTTGCTGTTTCAATTTTCAACCG	1198
DB	600	TGAGAGAGCTGAAAGGCTACTGAAATATATACCGGATATCTTTTTCATTTCAACCG	659
QY	1199	ATAAAGAAGCAGGCTCACCCAGGGAAGCTCAATACCACCTCCTTTCCAGAGTCTTTGCA	1258
DB	660	ATAAAGAGGATGSCACACCACTTGGTGAAGTTCAATGGCATCTCCATCTCCCTCTTGA	719
QY	1259	CTTTAGATCTGCCCTAGCAGCGTATGCTGATCTTTGAAATCTCTCTAGAAAGGCTTCTC	1318
DB	720	CTTTGGAACAGCAATGACTCGGTATGCTGATGTTTGGATTTCTCTCTCTCTCTCTCTT	779

QY	1319	TGATTGCTCTGTCGCTCATGTCATCTGTATCCAGTGAAGCAGAGAGATTGCGCTTTTGT	1378
DB	780	TACTTGTCTTTAGCGGATGTTCTTCTGATCCAAATGAAGCTGATCGATTAAAGATATCTAG	839
QY	1379	CATCACTCTGGGAAAGAATGAGTATTTCAAAATGGGTAGTTGGAAGTCAGAGAGTCTTT	1438
DB	840	CATCACTCTGGAAGGAAGAATATGCTCAGTGGATAGTTGCAAGTCAGAGAAGCCTTC	899
QY	1439	TGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGCTGCAG	1498
DB	900	TTGAAGTCAATGGCTGAATTTCTTTCAGCAAGCCTTCAATCGGTGTTTCTTTGCTTCTG	959
QY	1499	TAGCCCTCGCTTACCGCTCGATATCTTCTATCTCATCTCTCTCAAGTTTGGCTCCCT	1558
DB	960	TTGCTCTCGCTACCAACCAAGATTTCTACTCCATCTCATCACTCTCTAGATGCGGCGAT	1019
QY	1559	CAAGAATCATGTGACGTGTGTTTATGATATAGTTCAAAGCCCTACCGAAGGTTTCAACC	1618
DB	1020	CTAGAATTCATGTCACTTGTGCACTGGTTTACGACAAATGCAACTGGACGAATTCACA	1079
QY	1619	GAGGATGTTGCGACATGATGACATGCACTGCTCTCAGG--TA 1663	
DB	1080	AGGGTGTCTGCTCAACATGGAATGCTATCTCTCTAGAAAGAAAGCCTTTTCTCTGCA	1139
QY	1664	GCTGGGCTCTTATTTTGTTCGAACCTCAAACTTCAAGTTTACAGCTGACCCCTCAACTC	1723
DB	1140	GTACGCGCACTATTTTGTTCGCAATCAACTTTTAACTTGCAGCTGATTAACAAGTTTC	1199
QY	1724	CAATTATCATGTGGGACCTGTGTACAGGTAGTCTCTTTTACAGAGATTTTTCAGGAA	1783
DB	1200	CAATCATATGATTTGGCCCTGTGCTGATGATGTCACCACTTCAAGGCTTTTCTCAGGAA	1259
QY	1784	GAATGGCCCTCAAGGAAATGTTGCTCACTTGGCCACAGCTGCTCTTTTTCGATGTA	1843
DB	1260	GAATGGCTTGAAGGAGGAGCTGACCTTGGTCTCGAGTGTATTTTGGATGCA	1319
QY	1844	GGAATCGTAAATGGAATCTTATTAAGACGAACCTAAACAACTTCGTGGAAACGAGGAG	1903
DB	1320	GGACCGCAATGACTACATCTATCAGATGAGTTAGATTAATCTTCTTGGCCGCTG	1379
QY	1904	TCATTTGGAGCTAGTATTTGCTTTTACGTGGAAGGGGAAAGAGGAATATGTTCAAC	1963
DB	1380	CACCTTCTAATCTAGTTTGTGCTTCTCAGCTGAAGGACCTAAACAAAGAAATATGTCAAC	1439
QY	1964	ATAAGATGATGAGAAAGCAACGGATGATGGAATGATGATGATGATGATGATGATGATGAT	2023
DB	1440	ATAAATGACACAGAGAGGCGGACGATCTGGAACATGATTTCTCAGGAGGTTATGTTT	1499
QY	2024	ATGTGTGCTGATGCAAGGGAATGGCCAGAGATGCTCCATCGCAGTTGCAATACCATG	2083
DB	1500	ATGTGTGCTGATGCTAAGGCGATGGCCAGGATGCTCCATCGGACCTTTCACACTATTG	1559
QY	2084	CCCAAGAACAGGAGCCCATGGAATCATCTGCTGCGAAGCTGCAGTAAAGAACTCAAG	2143
DB	1560	CTCAGGATCAGGATCACTTGATAGCTCCCAAGGCGAGAGCTTTGTGAAGAATTTGCAAA	1619
QY	2144	TTGAAGACGATATCTTAAGAGATGTTGCTGATCG 2178	
DB	1620	CGACCGGAAGATATCTGCGTGTGATGTGTTGTAATG 1654	

RESULT 14
US-10-437-963-1516
; Sequence 1516, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 1516
LENGTH: 2136
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_101375C.1
US-10-437-963-1516

Query Match 28.4%; Score 751.6; DB 19; Length 2136;
Best Local Similarity 64.6%; Pred. No. 2.4e-185;
Matches 1211; Conservative 0; Mismatches 609; Indels 54; Gaps 4;
328 GAGGAGATTGAAGTTGATCCTGTAAATTAAGCTCACTATATTTTGGTACTCAGACT 387
199 GAGGAGCGCGCGCGCGGAGGAGGAGCGGCTCACCGTCTTCTTCGGCAGCAGACC 258
388 GGTACTGCTGAAGGATTTGCTAAGGCATTGGCAGAGAAATTAAGCAAGTACAGAAA 447
259 GGCACCGCGAGGCTTCGCCAAGGCACCTCGCTGAGAGGCTAAGTCAAGATACGACAAG 318
448 GCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCGGAGGATGATCAATATGAAGAG 507
319 GCGATATTCAAAGTTGTGGACTTTGGATGAGTATGCGATGCGGATGAGGAGTACGAGGAG 378
508 AAATTAAGAAAGACTCTTTGGTGTCTTTTCATGGTAGCCACTTATGGTGAATGGTAGCCA 567
379 AGATTCAAGAAAGAGAAGATATCGTTGTTCTTCGTTGCAACGCTACGAGATGGTGAACCG 438
568 ACTGACAAATGCTCGGAGATTTTACAATGGTTCACTCAGGAACATCAAAAGGGGAGAGTGG 627
439 ACTGACAAATGCTGCTAGGTTCTATAATGGTTCACTGAGGAAATGAGAGGGGTGTTGG 498
628 CTTACAGCAACTAATCTATGGTGTGTTTGGTTGGTAAACCGTCAATACGAGCATTTCAAC 687
499 TTGAATGACTTCCAGTATGCTATTTTGGCTTGGCAATCGGCAGTATGAGCATTTCAAC 558
688 AAGATCGCGGTAGATGGATGAGCAACTCGGTAAACAAGGTGCAAGCGCATTTGTTCAA 747
559 AAGGTTGCCAAGGTTGTGATGAGCTCCTAGTTGAGCAAGGTTGCAAAACGCTCTGTTCG 618
748 GTGGGCTCGGTGACGATGATCAATGCATTTGAAGATGATTTTACTGCTTGGCGAGAAATTG 807
619 GTTGGTCTTGGAGATGATGATCAATGCATTTGAGATGACTTCAACGCATGGAAAGAACT 678
808 TTGTGCACTGAATTTGGATCAGTTGCTCAAAGATGAGGATGCTGCTCCTTCAGTGGCTACA 867
679 CTCTGCCAGAAATTGGATCAGTTACTTTCGGGATGAAATGATGTTTCAACAGGCACTA-- 736
868 CCGTATATTGCTACTGTTCTGTAATACAGGATGATTCACGAACACTACGCTCGCGCT 927
737 -CTACACAGCTGCCATTCCTGAATACCGGTTTGAATTTGTTAAGCCTGATGAGGCGAGCC 795
928 CTGGATGATAAACAACATAATCTGCTAACGGGATGTTGCAATTTGATATTCTCCATCTCT 987
796 CATTTCGAGAGAAATTTCACTCTTGCAACAGGTTATGCGGTTTCATGATGCTCAGCATCT 855
988 TGAGAACCAATTTGCTCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGATAGATCCTGT 1047
856 TGCCGGGCCCAACGCTGCTGTCACGCGGAATCCACACTCTGCTTCTGATCGTTTCATGC 915
1048 ATACATCTCGAGTTCCACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATGTT 1107
916 ACTCATTTGGAGTTTACATATGCTGCGACCTGGCTTACGATATGAAACCCGTTGACCATGTT 975
1108 GGTGTTTATGCTGAGAACTCGCATGAAACTGTGCGAGGAAGCGGGAAGCTGTTGGGTCAA 1167

976 GGTGTATATACAGAGAACTGCGCTCGAGGTTGTAGAGAGGCGAGAGAGTTGTTAGGCTAC 1035
1168 CCCCTGGATTTGCTGTTTTCATATTCACAGGATAAAGAGAGCGGTCACCCC---AGGGA 1224
1036 TCCCCAGAGGCTTTTTCACCATCCATCGAGACAAAGAGACGGTACACCACTAGGTGGT 1095
1225 AGCTCATTTACAGCTCCTTTTCCAGGCTCTTGACACCTTACGATCTGCCCTCAGCACCTAT 1284
1096 GGTCTCTGGCTCCTCCATTCCTCCCGATTTACTGTGAGGAATCGGTTGCTAGATAT 1155
1285 GGTGATCTTTTGAATCCTCTAGAAAGGCTTCTCTGATTGCTCTGTCGCTCATGCTAT 1344
1156 GGGATCTTCTGATTTGCGCGAAGAGAGTGTCTTGGTTGCATTAGCTACTTATGCTTCA 1215
1345 GTACCCAGTGAAGCAGAGAGATTGCGCTTTTGTCTCATCACCTCTGGGAAGAAATGAGTAT 1404
1216 GATTCTACTGAAGCTGATCGTCTGAGGTTCTTGGGCTCTCCTGCTGGAAGGATGAGTAT 1275
1405 TCAAAATGGGTAGTTGGAAGTCAGAGGAGTCTTTTGGAGATCATGSCCGAGTTTCCATCA 1464
1276 GCTCAATGGGTTGTTCCGAGTCAAAAGAGTCTATTAGAAAGTATGAGCAGAGTTCCCTTCA 1335
1465 GCAAAACCCCTCTTGGTGTGTTCTTGTCTGAGTAGCCCTCGCTTACCGCTCGATAC 1524
1336 GCAAGCCTCCACTAGGAGTCTTCTTTCAGCGGTTGCTCTCGTCTTCAGCGGAGATAC 1395
1525 TATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTGCTTTA 1584
1396 TACTCAATTTCTTCACTAGCATGGCACCTACCAGAAATTCATGTTACATGTGCACCT 1455
1585 GTATATGTTCAAGCCCTACCGAAGGTTTACCGAGGAGTGTTCGACATGGATGAAG 1644
1456 GTCCATGAAAAAACCTCTGCGAAGGGTACATAAGGGAGTCTGCTCAACATGGATTAA 1515
1645 CATGCAAGTTCTCCAGGA-----TAGCTGGGCTCTTATTTTGTTCGAAACG 1689
1516 AATGCTATTTCCATCAGAGAGACAAAGGACTGCGAGCTGGGCTCCAGTTTGTGAGACAA 1575
1690 TCAAACTTCAAGTTTACCAGTCAACCTCACTCAATTTATCATGTGGGAGCTGTGTACA 1749
1576 TCAAACTTCAAACTGCTCTGATCCTTCAGTACCGGTTTATCATGATTTGGCCAGGAAC 1635
1750 GGGTTAGCTCTTTCAGAGGATTTCTGCAAGGAAGAAATGCGCCCTCAAGGAATGCTGCT 1809
1636 GGTCTGTCTCTTTCGCGGATTTCTTTCAGGAGAGGCTGCTCTCAAAAACAATCAGGAGCT 1695
1810 CAACTTGGCCAGCAGTGTCTTTTTTCGGATGTAGGAATCGTAATATGAGCTTCAATTTAT 1869
1696 GAGCTTGGTGGCTCGGATTTCTTCTTGGATCGAGAAACAGCAAGATGAGCTTCACTAT 1755
1870 GAAGACGAACATAAACAACCTTCTGGAACAGGAGTCAATTTTCGGAGCTAGTTATGCTTT 1929
1756 GAGGATGAGCTGAACAACCTTCTTTCAGGAAGGAGCATTTTCGAGCTGTTCTCGCTTC 1815
1930 TCAAGTGAAGGGGAAAGAGGAATATGTTTCAACATAGATGATGAGAAA----- 1980
1816 TCTCGTGAAGGCCCTTACGAAGGAATACGTCGAGCACAATAATGTGCGAGAAACGTTGCTCA 1875
1981 -----GCAACGGATGTATGGAATGTGATATCAGGGGACGGT 2016
1876 TATTTCTTACCTTTGCTGCTCAGGCTTCCGAAATCTGGGACATGATCTCCAGGGTGGT 1935
2017 TATCTCTATGTGTGTGATGCCAAGGGAATGGCCAGAGATGTCATCGACGTTGCAAT 2076
1936 TACATTTACGCTGTGTGTGATGCCAAGGATGGCCAGAGATGTACATAGAGTTCTCCAC 1995
2077 ACCATTTGCCAAGAACAGGACCCCATGGAATCATCTGCTGCCGAAGCTCGACGTAAGAAA 2136
1996 ACCATTTGACAGAACAGGATCACTTGACAGCTCTAAGGCTGAGAGCTTTGTGAAGAGC 2055
2137 CTCCAAGTTGAAGA 2150
2056 CTCCAAACGGAGGA 2069

RESULT 15

US-10-425-115-99832
; Sequence 99832, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 99832
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_22561C.1
US-10-425-115-99832

Query Match 28.3%; Score 750.8; DB 20; Length 2149;
Best Local Similarity 66.0%; Pred. No. 3.9e-185;
Matches 1142; Conservative 0; Mismatches 567; Indels 21; Gaps 3;

QY	464	TTGACCTGGATGACTGACGCGGAGGATGATCAATATGAGAGAAATTAAGAAAGAGT	523
DB	19	TGGTCGCGGTGTCTTCTGCTGCGGACCGCGCTGCTGCGGAGGAGGTGTAGGCCAGT	78
QY	524	CTTTGGTGTTCATGGTACGACCTATGCTGATGCTGATGCTGACCACTGACATGCTGCGA	593
DB	79	GGCTAGCGGTGTCTTCTGCTGCGCAACGATGAGATGCTGAGCGGACTGCAATGCTGCTA	138
QY	584	GATTTTACAAATGGTTCACACAGCAATCAAGAGGAGAGTGGCTTCAGCACTAACTT	643
DB	139	GGTTCACAAATGGTTCACAGGAAATGAGAGGAGTGGCTTCAGCACTAACTT	198
QY	644	ATCGTGTTCATGGTGTGGTAAACCGTCAATACGAGCATTTCAACAGATGCGCGGTAGATG	703
DB	199	ATCGTGTTCATGGTGTGGTAAACCGTCAATACGAGCATTTCAACAGATGCGCGGTAG	258
QY	704	TGATGAGCAACTCGGTAAACAGGTGCAAGGCGCATTTTCAAGTGGGGCTCGGTGACG	763
DB	259	TCGATGAGATTCCTGACAGAAACAAGGTGGAAAGCGCCTTGTTCAGTGTGGTCTTGGGAGC	318
QY	764	ATGATCAATGCTTGAAGATGATTTTACTGCTTGGCGAGAAATTTGTGGACTGAATTTGG	823
DB	319	ATGACCAATGCTTGAAGATGATTTTCAATGATGAGAAAGAGCTCTTGGCCAGAGTTGG	378
QY	824	ATCAGTTGCTCAAGATGAGGATGCTGCTCTTTCAGTGGCTACACCGTATATGCTACTG	883
DB	379	ATCGATTAATTCGGGATGAAATGATGCTCTCTCAGGCCCTACA---TACACAGCTGCAA	435
QY	884	TTCTGTAATACAGGTAGTGAATTCACGAACTAGGTGCGGGCTCTGGATGATAACACA	943
DB	436	TTCTGTAATACAGGTAGTGAATTCACGAACTAGGTGCGGGCTCTGGATGATAACACA	495
QY	944	TAAATACTGCTAACCGGATGTTGCAATTTGATATTTCTCCATCTTCAGAAACCATTTGG	1003
DB	496	TCAGCTTGAATGCGCATGAGTCCATGATGATGATGATGATGATGATGATGATGATGATG	555
QY	1004	CTCAACAAAGAGAGCTCCCAAAACCAAGCTGATGATGATGATGATGATGATGATGATG	1063
DB	556	TCGTGCGGAGGAACCTCCACACCCCTGCTTCTGATGCTTCTGATGCTTCTGATGCTT	615
QY	1064	ACATATCAGGCTCTTCCCTTACATATGAGCTGAGATCATGTTGTTGTTTATGCTGAGA	1123
DB	616	ACATATGCTGCACTGCTCACGATGATGAACTGGCGACCATGTTGGTGTATACACCGAGA	675

QY	1124	ACTGCGATGAACTGTCGAGGAAGCAGGAAAGCTGTTGGTCAACCCCTGGATTGCTGT	1183
DB	676	ACTGCGCTGAGGTTGTAGAGGAGGAGAGAGGTTGTTGGCTACTCGCCAGACACATTTT	735
QY	1184	TTTCAATTACACGGGATAAAGAGACGG---GTACCCCGAGGGAAGCTCATTTACCACCTC	1240
DB	736	TCACCATCCATGCAGACAAAGAGAGTGGCATTCTCAAGTGGCAGTTCTTCTGCTCCTC	795
QY	1241	CTTTCCCGAGTCTTTCACCTTACGATCTGCCCTAGCACGCTATGCTGATCTTTGATC	1300
DB	796	CGTTCCCTCCCAATCAGTGAAGAAATGCACTTGTAGATATGCGACCTTTCTAAAT	855
QY	1301	CTCCTAGAAAGGCTCTCTGATTGCTCTGTCGCTCATGCTGATACCCAGTGAAGCAG	1360
DB	856	CACCGAAGAGGCTCTCTGTTGCAATTAGCTTCTTATGCTTCAGATCTCTGCTGAGGCTG	915
QY	1361	AGAGATTGCGCTTTTGTCTATCACTCTCGGAAAGAAATGAGTATCAAAATGGGTAGTTG	1420
DB	916	ATCGTCTGAGGTTCTTGGCTCTGCTGCTGGCAAGGATGAGTATGCCAATGGGTTGTGG	975
QY	1421	GAGTCAGAGGAGTCTTTTGGAGATCATGCGCGAGTTTCCATCAGCAAAACCCCTCTTG	1480
DB	976	CAAGTCAGAGAGGCTGTTGGAAGTATGCGAGAGTTCCCTTCGCAAGCCCTCCATAG	1035
QY	1481	GTGTGTTCTTTGTCAGTAGCCCTCGCTTACCGCTCGATACTATTCTATCTCATCTT	1540
DB	1036	GAGTCTTCTTTGCGAGCTGTTGCCCCCTCGACTTCAACCAAGATATTTCTATTTCTAT	1095
QY	1541	CTCCTAAGTTTGTCTCCTCAAGAATTCATGTGACGTGTCTTTAGTATATGTTCAAAGCC	1600
DB	1096	CACCTAGTATGGCACCACAGGATTCATGTCACTGTGCGTCTGTCGCGCAAAACAACAC	1155
QY	1601	CTACCGAAGGCTTACCGAGAGTGTGTCGACATGATGAGCATGAGCTGCTCCTCAGG	1660
DB	1156	CGCTGGAAGGGTACATAAAGGGAGTTTGTCTCACTTGGATTAAGAAATGCTTCTTCGG	1215
QY	1661	A-----TAGCTGGGCTCTTATTTTGTTCGAACTCAAACTTCAAGTTAC	1705
DB	1216	AGGAGAGCAAGGATGCGAGCTGGCTCCGATATTTGTGAGGCAATCAAACTTCAAACTAC	1275
QY	1706	CAGCTGACCCCTCAACTCCAAATTCATGTTGGGAGCTGGTACAGGGTTAGTCTCTTTCA	1765
DB	1276	CGCTGATCTTTCAGTACCGATTCATGATTTGGCCCTGGGACCGGTCTTGCAACCTTCC	1335
QY	1766	GAGGATTTCTCAGGAAAGAAATGGCCCTCAAGGAAATGGTCTCAACTTGGCCCGAGCAG	1825
DB	1336	GTGGCTTCTTCAGGAAAGAAATTTGCTCAAAAGAAATCTGGAGCTGAGCTTGGTCTGAT	1395
QY	1826	TGCTCTTTTTCGATGTAGGAATCGTAATATGAGCTTCAATTTATGAAGACGAACTAAACA	1885
DB	1396	TGTTCTTCTTTGATGACAGAAACAGCAGATGAGCTTCACTATGAGGGGAGCTGACACA	1455
QY	1886	ACTTCGTGAAACGAGAGTCAATTCGAGCTAGTTATTCGCTTTTTCACGTGAAGGGGAAA	1945
DB	1456	ATTTCTGTCGAAAGAGAGCTGCTGAGCTGGTCTTCTGCTTCTCGCGCAGGGGCTTG	1515
QY	1946	AGAGGAATATCTTCAACATAGATGATGAGAAAGCAACGAGTGTATGGAATGCTGAT	2005
DB	1516	CTAAGGAATATGTCAGACACAAATGGCACAGAAAGCATCTGAAATCTGGGACATGATCT	1575
QY	2006	CAGGGGACGGTTATCTTATGTGTGTGTGATGCGCAAGGGAATGGCCAGAGATGTCATC	2065
DB	1576	CCCAAGGTGCTTACATCTATGCTGTGTGACGCGCAAGGCATGGCCAGAGAGTACATA	1635
QY	2066	GACGTTGCTATACCATTTGCCCAAGAACAGGACCCCATGGAATCATCTGCTGCCAAGCTG	2125
DB	1636	GAGTTCTCATACCATTTGTTCAAGGAGAGGGCTCCCTCGACACAGTTCTAAGGCCGAGAGCT	1695
QY	2126	CAGTAAGAACTCCCAAGTTGAAGACGATATCTAAGAGATGCTCTGCTGA	2175
DB	1696	TCGTGAAGAACTCCCAATGGAGGGGAGATATCTTGAGGATGTGTGTTAA	1745

Search completed: October 19, 2005, 16:45:29
Job time : 5870 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:55 ; Search time 8887 Seconds
(without alignments)
12168.363 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagctgttagtat.....ttttgaaaaa 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 45554873 seqs, 20411521753 residues
Total number of hits satisfying chosen parameters: 91109742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

1:	/cgn2_6/ptodata/1/pna/PCTUS1_COMB.seq.*
2:	/cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq.*
3:	/cgn2_6/ptodata/1/pna/PCTUS3_COMB.seq.*
4:	/cgn2_6/ptodata/1/pna/PCTUS4_COMB.seq.*
5:	/cgn2_6/ptodata/1/pna/PCTUS5_COMB.seq.*
6:	/cgn2_6/ptodata/1/pna/PCTUS6_COMB.seq.*
7:	/cgn2_6/ptodata/1/pna/PCTUS7_COMB.seq.*
8:	/cgn2_6/ptodata/1/pna/PCTUS8_COMB.seq.*
9:	/cgn2_6/ptodata/1/pna/PCTUS9_COMB.seq.*
10:	/cgn2_6/ptodata/1/pna/PCTUS10_COMB.seq.*
11:	/cgn2_6/ptodata/1/pna/PCTUS11_COMB.seq.*
12:	/cgn2_6/ptodata/1/pna/PCTUS12_COMB.seq.*
13:	/cgn2_6/ptodata/1/pna/PCTUS13_COMB.seq.*
14:	/cgn2_6/ptodata/1/pna/PCTUS14_COMB.seq.*
15:	/cgn2_6/ptodata/1/pna/PCTUS15_COMB.seq.*
16:	/cgn2_6/ptodata/1/pna/PCTUS16_COMB.seq.*
17:	/cgn2_6/ptodata/1/pna/PCTUS17_COMB.seq.*
18:	/cgn2_6/ptodata/1/pna/PCTUS18_COMB.seq.*
19:	/cgn2_6/ptodata/1/pna/PCTUS19_COMB.seq.*
20:	/cgn2_6/ptodata/1/pna/PCTUS20_COMB.seq.*
21:	/cgn2_6/ptodata/1/pna/PCTUS21_COMB.seq.*
22:	/cgn2_6/ptodata/1/pna/PCTUS22_COMB.seq.*
23:	/cgn2_6/ptodata/1/pna/PCTUS23_COMB.seq.*
24:	/cgn2_6/ptodata/1/pna/PCTUS24_COMB.seq.*
25:	/cgn2_6/ptodata/1/pna/PCTUS25_COMB.seq.*
26:	/cgn2_6/ptodata/1/pna/PCTUS26_COMB.seq.*
27:	/cgn2_6/ptodata/1/pna/PCTUS27_COMB.seq.*
28:	/cgn2_6/ptodata/1/pna/PCTUS28_COMB.seq.*
29:	/cgn2_6/ptodata/1/pna/PCTUS29_COMB.seq.*
30:	/cgn2_6/ptodata/1/pna/PCTUS30_COMB.seq.*
31:	/cgn2_6/ptodata/1/pna/PCTUS31_COMB.seq.*
32:	/cgn2_6/ptodata/1/pna/PCTUS32_COMB.seq.*
33:	/cgn2_6/ptodata/1/pna/PCTUS33_COMB.seq.*
34:	/cgn2_6/ptodata/1/pna/PCTUS34_COMB.seq.*
35:	/cgn2_6/ptodata/1/pna/PCTUS35_COMB.seq.*
36:	/cgn2_6/ptodata/1/pna/PCTUS36_COMB.seq.*
37:	/cgn2_6/ptodata/1/pna/PCTUS37_COMB.seq.*
38:	/cgn2_6/ptodata/1/pna/PCTUS38_COMB.seq.*
39:	/cgn2_6/ptodata/1/pna/PCTUS39_COMB.seq.*
40:	/cgn2_6/ptodata/1/pna/PCTUS40_COMB.seq.*
41:	/cgn2_6/ptodata/1/pna/PCTUS41_COMB.seq.*
42:	/cgn2_6/ptodata/1/pna/PCTUS42_COMB.seq.*
43:	/cgn2_6/ptodata/1/pna/PCTUS43_COMB.seq.*

44:	/cgn2_6/ptodata/1/pna/US099F_COMB.seq.*
45:	/cgn2_6/ptodata/1/pna/US099G_COMB.seq.*
46:	/cgn2_6/ptodata/1/pna/US100A_COMB.seq.*
47:	/cgn2_6/ptodata/1/pna/US100B_COMB.seq.*
48:	/cgn2_6/ptodata/1/pna/US101A_COMB.seq.*
49:	/cgn2_6/ptodata/1/pna/US101B_COMB.seq.*
50:	/cgn2_6/ptodata/1/pna/US102A_COMB.seq.*
51:	/cgn2_6/ptodata/1/pna/US102B_COMB.seq.*
52:	/cgn2_6/ptodata/1/pna/US103A_COMB.seq.*
53:	/cgn2_6/ptodata/1/pna/US103B_COMB.seq.*
54:	/cgn2_6/ptodata/1/pna/US104A_COMB.seq.*
55:	/cgn2_6/ptodata/1/pna/US104B_COMB.seq.*
56:	/cgn2_6/ptodata/1/pna/US105A_COMB.seq.*
57:	/cgn2_6/ptodata/1/pna/US105B_COMB.seq.*
58:	/cgn2_6/ptodata/1/pna/US106A_COMB.seq.*
59:	/cgn2_6/ptodata/1/pna/US106B_COMB.seq.*
60:	/cgn2_6/ptodata/1/pna/US107A_COMB.seq.*
61:	/cgn2_6/ptodata/1/pna/US107B_COMB.seq.*
62:	/cgn2_6/ptodata/1/pna/US107C_COMB.seq.*
63:	/cgn2_6/ptodata/1/pna/US107D_COMB.seq.*
64:	/cgn2_6/ptodata/1/pna/US108A_COMB.seq.*
65:	/cgn2_6/ptodata/1/pna/US108B_COMB.seq.*
66:	/cgn2_6/ptodata/1/pna/US109A_COMB.seq.*
67:	/cgn2_6/ptodata/1/pna/US109C_COMB.seq.*
68:	/cgn2_6/ptodata/1/pna/US110_COMB.seq.*
69:	/cgn2_6/ptodata/1/pna/US6000_COMB.seq.*
70:	/cgn2_6/ptodata/1/pna/US6001_COMB.seq.*
71:	/cgn2_6/ptodata/1/pna/US6002_COMB.seq.*
72:	/cgn2_6/ptodata/1/pna/US6003_COMB.seq.*
73:	/cgn2_6/ptodata/1/pna/US6004_COMB.seq.*
74:	/cgn2_6/ptodata/1/pna/US6005_COMB.seq.*
75:	/cgn2_6/ptodata/1/pna/US6006_COMB.seq.*
76:	/cgn2_6/ptodata/1/pna/US6007_COMB.seq.*
77:	/cgn2_6/ptodata/1/pna/US6008_COMB.seq.*
78:	/cgn2_6/ptodata/1/pna/US6009_COMB.seq.*
79:	/cgn2_6/ptodata/1/pna/US6010_COMB.seq.*
80:	/cgn2_6/ptodata/1/pna/US6011_COMB.seq.*
81:	/cgn2_6/ptodata/1/pna/US6012_COMB.seq.*
82:	/cgn2_6/ptodata/1/pna/US6013_COMB.seq.*
83:	/cgn2_6/ptodata/1/pna/US6014_COMB.seq.*
84:	/cgn2_6/ptodata/1/pna/US6015_COMB.seq.*
85:	/cgn2_6/ptodata/1/pna/US6016_COMB.seq.*
86:	/cgn2_6/ptodata/1/pna/US6017_COMB.seq.*
87:	/cgn2_6/ptodata/1/pna/US6018_COMB.seq.*
88:	/cgn2_6/ptodata/1/pna/US6019_COMB.seq.*
89:	/cgn2_6/ptodata/1/pna/US6020_COMB.seq.*
90:	/cgn2_6/ptodata/1/pna/US6021_COMB.seq.*
91:	/cgn2_6/ptodata/1/pna/US6022_COMB.seq.*
92:	/cgn2_6/ptodata/1/pna/US6023A_COMB.seq.*
93:	/cgn2_6/ptodata/1/pna/US6023B_COMB.seq.*
94:	/cgn2_6/ptodata/1/pna/US6024_COMB.seq.*
95:	/cgn2_6/ptodata/1/pna/US6025_COMB.seq.*
96:	/cgn2_6/ptodata/1/pna/US6026_COMB.seq.*
97:	/cgn2_6/ptodata/1/pna/US6027_COMB.seq.*
98:	/cgn2_6/ptodata/1/pna/US6028_COMB.seq.*
99:	/cgn2_6/ptodata/1/pna/US6029_COMB.seq.*
100:	/cgn2_6/ptodata/1/pna/US6030_COMB.seq.*
101:	/cgn2_6/ptodata/1/pna/US6031_COMB.seq.*
102:	/cgn2_6/ptodata/1/pna/US6032_COMB.seq.*
103:	/cgn2_6/ptodata/1/pna/US6033_COMB.seq.*
104:	/cgn2_6/ptodata/1/pna/US6034_COMB.seq.*
105:	/cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
106:	/cgn2_6/ptodata/1/pna/US6036_COMB.seq.*
107:	/cgn2_6/ptodata/1/pna/US6037_COMB.seq.*
108:	/cgn2_6/ptodata/1/pna/US6038_COMB.seq.*
109:	/cgn2_6/ptodata/1/pna/US6039_COMB.seq.*
110:	/cgn2_6/ptodata/1/pna/US6040_COMB.seq.*
111:	/cgn2_6/ptodata/1/pna/US6041_COMB.seq.*
112:	/cgn2_6/ptodata/1/pna/US6042_COMB.seq.*
113:	/cgn2_6/ptodata/1/pna/US6043_COMB.seq.*
114:	/cgn2_6/ptodata/1/pna/US6044_COMB.seq.*
115:	/cgn2_6/ptodata/1/pna/US6045_COMB.seq.*
116:	/cgn2_6/ptodata/1/pna/US6046_COMB.seq.*

THIS PAGE BLANK (USPTO)

117: /cgn2_6/ptodata/1/pna/US6047 COMB.seq.*
 118: /cgn2_6/ptodata/1/pna/US6048 COMB.seq.*
 119: /cgn2_6/ptodata/1/pna/US6049 COMB.seq.*
 120: /cgn2_6/ptodata/1/pna/US6050 COMB.seq.*
 121: /cgn2_6/ptodata/1/pna/US6051 COMB.seq.*
 122: /cgn2_6/ptodata/1/pna/US6052 COMB.seq.*
 123: /cgn2_6/ptodata/1/pna/US6053 COMB.seq.*
 124: /cgn2_6/ptodata/1/pna/US6054 COMB.seq.*
 125: /cgn2_6/ptodata/1/pna/US6055 COMB.seq.*
 126: /cgn2_6/ptodata/1/pna/US6056 COMB.seq.*
 127: /cgn2_6/ptodata/1/pna/US6057 COMB.seq.*
 128: /cgn2_6/ptodata/1/pna/US6058 COMB.seq.*
 129: /cgn2_6/ptodata/1/pna/US6059 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:52 ; Search time 12772 Seconds
(without alignments)
2923.857 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagctttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 26893129 seqs, 7048604437 residues

Total number of hits satisfying chosen parameters: 53786258

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New:
1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:
2: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:
3: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:
4: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:
5: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:
6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:
7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:
8: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:
9: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
10: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
11: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
12: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
13: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
14: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
15: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
16: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
17: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
18: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
19: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:
20: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
21: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
22: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
23: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
24: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
25: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
26: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq:
27: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID

THIS PAGE BLANK (01SEP70)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:52 ; Search time 7650 Seconds

(without alignments)
13180.686 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479087

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	978.8	36.9	2343	CNS0A2GR	EX827429 Arabidops
2	875.8	33.1	2362	CNS0A2GR	EX827591 Arabidops
3	640.2	24.2	1813	AY103952	AY103952 Zea mays
4	460.8	17.4	1596	CL969868	CL969868 OAFIC019
5	433.4	16.4	876	CB976975	CB976975 CAB40003
6	428.8	16.2	835	CO163167	CO163167 FLD1_39_H
7	426.4	16.1	893	CO254258	CO254258 NS00821-B
8	421	15.9	806	CO166163	CO166163 FLD1_59_F
9	419.2	15.8	907	CO084955	CO084955 GR_Ea01N
10	418.8	15.8	928	CK271587	CK271587 EST717665
11	415	15.7	855	CO368449	CO368449 RTK1_40_E
12	413.8	15.6	729	BM535223	BM535223 EST58245
13	413.6	15.6	690	BU813507	BU813507 N011C09_P
14	412.2	15.6	853	CNS49512	CNS49512 G00241.B3
15	411	15.5	824	CO109078	CO109078 GR_EB004
16	405.6	15.3	763	B1923088	B1923088 EST542992
17	394.4	14.9	659	A1730999	A1730999 BNIGH1837
18	394	14.9	775	BF003997	BF003997 EST432486
19	393.4	14.9	837	CN125396	CN125396 RHOH1_10
20	387.8	14.6	793	CN189862	CN189862 UCRCS06_0
21	387.6	14.6	782	CNS20768	CNS20768 G00106.B3
22	387	14.6	867	CF832302	CF832302 UCRCS02_0
23	383.8	14.5	837	CO368300	CO368300 RTK1_39_G
24	381.2	14.4	647	CF418771	CF418771 USDA_FP_1

25	380.2	14.4	846	6	CB670323	CB670323 OSJN5e03F
26	380	14.3	670	7	CF542988	CF542988 S014680W-
27	380	14.3	857	6	CD438804	CD438804 ELO105U17
28	379.8	14.3	849	6	CA289299	CA289299 SCCFLU800
29	379.6	14.3	843	7	CO199633	CO199633 G002_2_C0
30	378.4	14.3	710	6	CA159247	CA159247 SCJFR23C0
31	378.2	14.3	659	2	AW695744	AW695744 NF098803S
32	377.6	14.3	858	7	CF832300	CF832300 UCRCS02_0
33	371.4	14.0	658	2	AW236561	AW236561 EST304698
34	370.6	14.0	750	7	CO166517	CO166517 FLD1_62_C
35	369.2	13.9	848	7	CO132719	CO132719 GR_Eb45L
36	366.6	13.8	683	2	AW398515	AW398515 EST309015
37	366	13.8	767	6	CA158489	CA158489 SCEZR2309
38	366	13.8	927	7	CO201857	CO201857 RGN23_8
39	365.2	13.8	777	6	CA157581	CA157581 SCEZR2301
40	364	13.7	692	7	CO158240	CO158240 FLD1_5_C0
41	361.2	13.6	599	6	CB007356	CB007356 VVC044D08
42	359.4	13.6	791	7	CO362574	CO362574 RTK1_4_A0
43	358.6	13.5	705	6	CA099956	CA099956 SCVPC1604
44	358	13.5	783	7	CF447166	CF447166 EST683511
45	357.6	13.5	824	4	EG319913	EG319913 Zm03_08d1

ALIGNMENTS

RESULT 1	CNS0A2GR	2343 bp	linear	HTC 06-FEB-2004
CNS0A2GR	Arabis thaliana Full-length cDNA Complete sequence from clone			
LOCUS	GSJLSS32F02 of adult vegetative tissue of strain col-0 of			
DEFINITION	Arabis thaliana (thale cress).			
ACCESSION	EX827429			
VERSION	EX827429.1 GI:42459921			
KEYWORDS	HTC; GSJL cDNA.			
SOURCE	Arabis thaliana (thale cress)			
ORGANISM	Arabis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis;			
	1 (bases 1 to 2343)			
	Castelli V., Aury J.M., Jaillon O., Wincker P., Clepet C.,			
	Menard M., Cruaud C., Quetier F., Scarpelli C., Schachter V.,			
	Temple G., Caboche M., Weissenbach J., and Salanoubat M.			
TITLE	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:			
	A Combined Approach to Evaluate and Improve Arabidopsis Genome			
JOURNAL	Annotation			
REFERENCE	Unpublished			
AUTHORS	2 (bases 1 to 2343)			
TITLE	Genoscope.			
JOURNAL	Direct Submission			
	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :			
	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
	- Web : www.genoscope.cns.fr)			
COMMENT	The sequences are based on single pass reads			
	Life Technologies (a division of Invitrogen) members carried out			
	full-length libraries construction : Temple G.			
	Genoscope members carried out sequencing and annotation : Castelli			
	V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,			
	Schachter V., Weissenbach J., Salanoubat M.			
	URGV INRA : Clepet C., Caboche M.			
	Annotation is based on the June 2003 version of the Arabidopsis			
	genome released by MIPS (Munich Information center for Protein			
	Sequences) . 5 prime and 3 prime are assembled with Phrap.			
	http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full			
	length			
	http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.			
FEATURES	Location/Qualifiers			
source	1..2343			
	/organism="Arabidopsis thaliana"			
	/mol_type="mRNA"			
	/strain="Col-0"			
	/db_xref="taxon:3702"			

/clone="GSLTSL532F02"		/tissue_type="Adult vegetative tissue"	
Best Local Similarity 71.1%; Pred. No. 1.1e-258;		complement (1. .2343)	
Matches 1344; Conservative 0; Mismatches 527; Indels 19; Gaps 3;		/gene="At4g24520"	
ORIGIN			
Query Match	36.9%; Score 978.8; DB 3; Length 2343;		
Best Local Similarity	71.1%; Pred. No. 1.1e-258;		
Matches 1344; Conservative	0; Mismatches 527; Indels 19; Gaps 3;		
QY	310 ATAAATGATAAAGAAGAGAGAGATTGAAGTTGATCCCTGGTAAATTAAGCTCACTATA	369	1167 GGTCCCCATTGGAAAGCCAGTGGCGCTCTCTTCCCTGGTCCATGCACACTTGGGACT
DB	271 ATGGCTAAGACGAGAGATGATGATTGGATTGGGATCCGGGAAGACTAGAGTCTCTATC	330	1270 GGCCTAGCAGCTATGCTGATCTTTTGAATCTCTCTAGAAAGCTTCTCTGATTTGCTCTG
QY	370 TTTTGTGGTACTCAGACTGGTACTGCTGAAAGGATTTGCTAAGGCAATTGGCAGAAGAAATT	429	1227 GGTTTGGCAAGATACGCAGACCTTTTGAACCTCTCTCGAAAGTCTGCGTTAGTTGCTTGG
DB	331 TTCTTCGGTACGAGACTGGAACAGCTGAGGATTTGCTAAGGCATTATCCGAAGAAATC	390	1330 TCGCTCATGCTATCTGTACCCAGTGAAGCAGAGAGATTGGGCTTTTGTTCACACCTCTG
QY	430 AAGGCAAAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGATGACTATGACGCGAG	489	1287 GGGGCTATGGCCTATGGCCTGAACCAAGTGAAGCCGAGAACTTTAAGACCTGACATCACCTGAT
DB	391 AAAGCGAGATATGAAAAGAGCAGCTGAGGATTTGCTAAGGCATTATCCGAAGAAATC	390	1390 GGAAGAAATGAGTATTCAAAATGGGTAGTTGGAAGTCAAGAGAGTCTTTTGGAGATCATG
QY	490 GATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTGGTGTGTTTTCATGTTAGCCACT	549	1347 GGAAGAGTGAAGTACTCAATGGATTGTTGCAAGTCAAGAGAGTCTTTTAGAGGTGATG
DB	451 GATGACCAATATGAAGAGAAATTAAGAAAGAACTTTGGCATTTTTCGTGTGTTGCTACT	510	1450 GCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTGTCTGCAAGTCCCTCGC
QY	550 TATGGTGATGGTGAGCCAACTGACAAATGCTGCGAGATTTTACAAATGGTTCACTCAGGAA	609	1509 GCTGCTTTTCCATCTGCAAAACCCCTAGGTGTATTTTGTCTGCAATAGTCTCTCGT
DB	511 TATGGAGATGAGAGCTCTGACAAATGCTGCCAGATTTTACAAATGGTTTACGGAGGAA	570	1510 TTACGCCCTCGATACTATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCAT
QY	610 CATGAAGGGGAGTGGCTTACGAACTAACTTATGAGTGTGTTTGGTGTGTTTGGTGTACCGT	669	1467 CTACAACTCTGTTACTTACTTCTCATCTCGCCAAAGATTGGCGCAAGTAGAGTTTCAAT
DB	571 AATGAACGGGATATAAGCTTCAACAACTAGCATATGTTGTTGTTGTTCTTGTGTAATCGC	630	1570 GTGACGTGTGTTTGTATATGTTCAAGCCCTACCGGAAGGTTTCAACGAGGAGTGTGT
QY	670 CAATACGAGCATTTCAACAGATCGGCTAGATGCTGATGAGCAACTCGTAAACAGGT	729	1527 GTTACATCCGACTAGTATATGTTCCAACTCTCTACTGTGTAAGTCCACAAGGTTGTGT
DB	631 CAATATGAACATTTTATAAGATCGGATAGTTCTTGATGAAGATTATGTAAGAGAGGT	690	1630 TCGACATGGATGAAGCATGAGTTCTCTCAGGA-----TAGCTGGGTCTCT
QY	730 GCAAAGCGCATTTTCAAGTGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTT	789	1587 TCTACGTGATGAAGAAATGAGTTCTCGCGAGAAAGTCAATGATGTAGTGGAGCCCCA
DB	691 GCAAAGCGTCTTATTTGAAGTCCGCTTAGGAGATGATGATCAGAGCATTTGAGGATGATTTT	750	1675 ATTTTGTTCGAAACGTCGAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTTATCATG
QY	790 ACTGCTTGGCGAGAAATTTGTGAGTCAATTTGATGAGTGTGCTCAAGATGAGGATGCT	849	1647 ATCTTTATTCGAGCATCTAAATTTCAAGTTTACCATCCAACTTCAACTCCAATCGTTATG
DB	751 GATGCTTGGAAAGATCACTATGTTGCTGAGCTAGACAAAGCTCTCAAGACGAGGATGAT	810	1735 GTGGGACCTGTTACAGGGTTAGTCTCTTTTCAAGAGATTCTGCGAGAAAGAAATGGCCCTC
QY	850 GCTCTTTCAGTGGCTACACGCTATATTTGCTGTTCTTGAATACAGGTTAGTTCAC	909	1707 GTGGGACCTGGGACTGGGCTGGCACCTTTTAGAGGTTTCTGCGAGAAAGGATGGCACTA
DB	811 AAGAGT---GTGGCACTCTTATACAGCTGTTATTCCTGAAATACCGGTGGTGAATCAT	867	1795 AAGGAAATTTGTTGCTCAACTGGCCGACAGTGTCTTTTTCGGATGTAGGAAATCGTAAAT
QY	910 GAAACTACGCTCGGGCTCTGGATGATGAACACATAAATCTGCTAACCGCGATGTTGCA	969	1767 AAGAAGATGGAGAGAACTAGGTTTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
DB	868 GATCCTCGTTTACAACCTCAAAATCAATGGGATCAGATGTTGGCAATGGGATGCTACT	927	1855 ATGGACTTTCATTTATGAAGACGAACTTAAACAACTCTGCGAAACGAGAGTCAATTTCCGGAG
QY	970 TTTGATATTCCTCATCTTTCAGAACCAATTTGTTGCTCAACAAAGAGAGCTTCCAAACCC	1029	1827 ATGGACTTATATACAGGATGAGCTCAATATTTTGTGATCAAGGCGGATATATCTGAG
DB	928 ATTGACATTCCTCATCTCCCTCAGAGTTGATGTTGCTGTGAGAAAGGGGCTTCCACACAT	987	1915 CTAGTTTATTTGCTCTTTTCACTGAAAGGGGAAAGAGAAATATGTTTCAACATAGATGATG
QY	1030 AAGTCTGATAGATCTGATACATCTGAGTTCGAGATATCAGGCTCTTCCCTTTACATAT	1089	1887 CTATCATGCGCATTTCTCCGTGAAGGAGCTCAGAAGGATATGTTTCAACATAGATGATG
DB	988 GAATCTGAT--GGTCTTGATCTCATCTGAGTTGACATATCCAGGAGCGGATATACATAT	1046	1975 GAGAAAGCAACGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGT
QY	1090 GAGACTGGAGATCATGTTGTTTATGCTGAGAACTGCGATGAAACTGTGCGAGGAGCA	1149	1947 GAGAAGGACGACCAAGTTTGGGATCTAATAAAGGAAAGAGGATATCTCTATGTATGCGGT
DB	1047 GAAACAGGTGACCATGTAGGTGATATGCTGAAATCATGTTGAAATGAGTTGAAGAAGCT	1106	2035 GATGCCAAGGGAATGGCCAGAGATGTCATCCACGTTCCATACCATACCTGCCCAAGAACAG
QY	1150 GGAAGCTGTGGGTCAACCCCTGGATTGCTGTTTTCATTTCAATTCACAGGATTAAGAGAC	1209	2007 GATGCTAAGGGCATGGCGAGGAGCTCCACCGAACTCTCACACCACTTTTTCAGGAGCAG
DB	1107 GGAATAATTTGCTGGCCACTCTTTAGATTTTGTAGTATTTTCCATCATGCTGAACAAGGAGAT	1166	2095 GGAACCATCGAATCATCTGCTCGGAAAGCTGAGTAAAGAAACTCCAAAGTTGAAGAACGA
QY	1210 GGGTCAACCCGAGGAGCTCATTTACCACTCTCTTCCAGGCTCTTCCAGCTTTACGATCT	1269	2067 GAAGGTGTGAGTTGCTCAGAGGACAGAGGCTATAGTTAAGAACTTCAAAACCGAAGAGA

RESULT 2
CNS0A2CR
LOCUS

Arabidopsis thaliana Full-length cDNA complete sequence from clone
GSLTSL572C12 of Adult vegetative tissue of strain col-0 of
Arabidopsis thaliana (thale cress).

CNS0A2CR 2362 bp mRNA linear HTC 06-FEB-2004


```
Db 791 AGTTTATGGCCCTTCCACCAACAGAGGATCCACCAAGAGTTTGTTCACATGGATGAA 850
Qy 1644 GCATGAGTTCTCAGGA-----TAGCTGGCTCCCTATTTTGTGTAAC 1688
Db 851 GAATACAAATTCCTCTGGAATATAGCGAAGATGAGCTGGCTCCCATATTTGAGGCA 910
Qy 1689 GTCAAACTTCAAGTTACAGCTGACCCCTCAACTCCAAATTCATGCTGGGACTGTATC 1748
Db 911 GTCAATTTCAAGTTACTGCTGATCTGTCTCACTCCGATTCATGATGCTCTGAGAC 970
Qy 1749 AGGTTAGTCTCTTTCAGAGATTTCTGCAAGAAAGAAATGCCCTCAAGGAAAATGTGC 1808
Db 971 AGGCTGGCTCCTTTTAGAGGCTTCTTGCAAGAAAGGTAGCATTTGAAACAACTCGGAGC 1030
Qy 1809 TCAACTTGGCCAGCAGTCTCTTTTCGAGATGTAGGAATCGTAATATGCACTTCATTA 1868
Db 1031 AGAATGGGCACATTCATCCCTTTTCTTGGATCGAGAACCGTAATATGGAATACATATA 1090
Qy 1869 TGAAGACGAACTAAACAACTTCTGGAACCGAGAGTCAATTTCCGAGCTAGTTATGCTT 1928
Db 1091 TGAAGATGAGTTGCAAACTTCTTGAAGAGGGGCGCTTCTGAGCTAATTTGTGCAAT 1150
Qy 1929 TTCACTGGAAGGGGAAAGAGGAATATGTTCAACATPAAGATGATGGAGAAAGCAACGGA 1988
Db 1151 CTCTCGGGAAGGCCAACGAAGAAATATGTGCAAGATAAGATGGTGGAAAGGCCACAGA 1210
Qy 1989 TGTATGGAATGTATATCAGGGAGCGTTATCTCTATGTGTGTGATGATCCCAAGGAAT 2048
Db 1211 TATTTGGAACATCATCTCAGATGGTGTATCTTATATGATGCGGTGATGCCAAGGGAAT 1270
Qy 2049 GGCAGAGATGTCCATCGCAGTTGCATACCATTTGCCAAGAACACAGGACCCATGGAATC 2108
Db 1271 GGCAGAGATGTACACAGGATGCTTCAATAGTAGTCCAGAGACAGGATCTTTGGATAG 1330
Qy 2109 ATCTGCTCCGAAAGCTGCAGTAAGAACTCCAAGTTTGAAGAACGATATCAAGAGATGT 2168
Db 1331 CTCACAAACCGAGAGCTACGTAAGAGCCTGCAGATGGAAGGAGGTACCTCGTGATGT 1390
Qy 2169 CTGGTGA 2175
Db 1391 ATGGTGA 1397

RESULT 4
CL969868
LOCUS
DEFINITION
CL969868 1596 bp DNA linear GSS 21-SEP-2004
OaIFCC019063 Oryza sativa Exprim Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION
CL969868
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1596)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
```

```
FEATURES
source
Location/Qualifiers
1..1596
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Exprim Library"
/notes="Oryza sativa exon trapped genomic sequences"

ORIGIN
Query Match 17.4%; Score 460.8; DB 9; Length 1596;
Best Local Similarity 66.9%; Pred. No. 1.7e-115;
Matches 673; Conservative 0; Mismatches 327; Indels 6; Gaps 1;

Qy 400 GGAATTTGCTAAGGCATTTGGCAGAAAGAAATTTAAGGCCAAAGTACAAAGAAAGCAGTTGTTAAA 459
Db 148 GGTTCGATCCGGCGATGGCAGAGGAGGCGGCGGTACGAGAAAGCGGTGTTCAA 207
Qy 460 GTAGTTGACCTGGATGACTATGAGCCGAGGATGATCAATATGAAGAGAAATTTAAAGAAA 519
Db 208 GTTGTGATCTGGATGACTATGAGCTGAGGATGAGGAGTACGAGGAGAGCTCAGGAAG 267
Qy 520 GAGTCTTTGGTGTTCATGTGTAGCCACTTATGTGTAGTGTGAGCACTGAGCAACTGCAATGCT 579
Db 268 GAAACTATCGTGTGCTCTTCTTAGCAACATATGGGGATGGGAGCGCTACCGCAATGCT 327
Qy 580 GCGAGATTTTACAAATGGTTTCACTCAGGAACATGAAAGGGAGAGTGGCTTTCAAGCAACTA 639
Db 328 GCAAGATTTTACAAATGGTTTCACTGAGGGAGAGAAAGAAAGTCTGGCTTTAAGGATCTT 387
Qy 640 ACTTATGGTGTTCCTTGGTAAACCGTCAATACGAGCATTTCAACAGATCGCGGTA 699
Db 388 AAGTATGCTGTTCCTGGCTGGGAAATAGGCAGTATGAGCACATTTAATAGGTTGCAAG 447
Qy 700 GATGTGATGAGCACTCGGTAAACAGGTGCAAGGCAATTTTCAAGTGGGCTCGGT 759
Db 448 GTGGTGGAGCAACTGTCTAGAGGAGGAGGTGGCAAGCGTCTTGTCCAGTTGGCTTGA 507
Qy 760 GAGCATGATCAATGCAATGAAGATGATTTTACTGCTTGGCGAGAAATTTGTTGAGCTGAA 819
Db 508 GATGATGATCAGTGATTCAGGATGATCTTCAAGCATGGAAGAACAGTTTGGCCAGAA 567
Qy 820 TTGGATCAGTTGCTCAAAGATGAGGATGCTGCTTCTCAGTGGCTACACCGTATATTGCT 879
Db 568 TTGGACCAACTGCTCGTGTGATGAAGATGATACAACTGGTGTGCTCCTTACACTGCT 627
Qy 880 ACTGTTCTGAATACAGGGTAGTGTATTCAGAAACCTACGGTCCGCGCTCTGGATGATAA 939
Db 628 GCTATACCTGAATACAGAAATTTGATTTATTTGATAAATCAGATGATATCGTTTCAAGACAA 687
Qy 940 CACATAAATACGTCTAAACGGCATGTTGCATTTGATATTTCTCCATCCTTCAGAACCAT 999
Db 688 TCGTGTCTCTTCCCAATGGCAGTGGTGTATTTGATATTTACCATCTCTGTCAAGTCTAAT 747
Qy 1000 GTTGTCTCAAAGAGAGAGCTCCAAACCAACCAAGCTCTGTAGATGCTCTGTATACATCTGGAG 1059
Db 748 GTTGTCTTTCGAAAGGAACTCCATAAGCAGCTTCAGATCGCTCTTGTGATTCATCTGGAG 807
Qy 1060 TTCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATGTTGGTGTATTGCT 1119
Db 808 TTGATATCTCAGGCACTGCTCTTGTGTATGAACTGGTGACCATGTTGGTGTATTATCA 867
Qy 1120 GGAACCTGGGATGAAACTGTGAGGAGGAGGAGGAGCTGTGGGTCAACCCCTGGATTG 1179
Db 868 GAAATGCTATTCGAGACAGTGGGAGGAGGCTGAAAGCTGTAGATCTTTTCCAGATACA 927
Qy 1180 CTGTTTTCATTTTCAACCGGATGAAGAGCGGTGCTACCCC-----AGGGAAGCTCATTA 1233
Db 928 TTTTCTCCGTCCATGCAGACGCGAGAGATGGATCACTCTGTAAGAGGGGTGGTCTTTG 987
Qy 1234 CCACTCTCTTCCAGGTCCTTGCACCTTACGATCTGCGCTAGCAGCTGTGCTGATCTT 1293
Db 988 GCCCCACCTTTCCCTTCTCCTTGCACCTTACCGAGCTGCACCTTCTAAGATATGCTGATCTA 1047
```

```
QY 1294 TTGAATCCTCTAGAAAGGCTTCTCTGATGCTCTGCTCCGCTCATGCACTGTACCAGT 1353
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1048 CTTAAATCTCCAAGAAGGCTGCTTGGTGTGCTTTAGCTCTCTCATGCTGTGACCTAGCT 1107
QY 1354 GAAGCAGAGAGATGGCGCTTTTGTGTCATCACTCTCGGAAGAATG 1399
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1108 GAAGCTGAAGATGAGATTTTGGCTTCCCTCTCGGAAGGATG 1153

RESULT 5
CB976975 876 bp mRNA linear EST 01-MAY-2003
LOCUS CAB40003.Ila_Fa_B09 Cabernet Sauvignon Berry - CAB4 Vitis vinifera
DEFINITION cDNA clone CAB40003.Ila_Fa_B09 5', mRNA sequence.
ACCESSION CB976975
VERSION 1
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 876)
AUTHORS Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leellie,A., Xu,J.,
Jones,K. and Cook,D.
TITLE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
FEATURES
    source
        1..876
            /organism="Vitis vinifera"
            /mol_type="mRNA"
            /cultiivar="Cabernet Sauvignon"
            /db_xref="taxon:29760"
            /clone="CAB40003.Ila_Fa_B09"
            /sex="Hermaphrodite"
            /dev_stage="Berry on stage II, 9 mm"
            /lab_host="DH5alpha"
            /clone_lib="Cabernet Sauvignon Berry - CAB4"
            /notes="Organ: Berry; Vector: pDNR; Site 1: Sfil; Site 2:
            Sfil; CAB4 is a cDNA library of Vitis vinifera cv.
            'Cabernet Sauvignon' Clone 8 berries. Sampled berries were
            collected from field-grown vines during stage II of berry
            growth (berries were green and hard) at approximately 60
            days after full bloom.The average berry size was 9
            millimeters. Sampled vines were located at the University
            of California, Davis, Experimental Vineyard. cDNAs were
            made by oligo-dT priming and directionally cloned. 5' and
            3' adaptors were used in cloning as follows:
            5'-AAGCATGGTATCAAGCAGAGTGGCCATTACGCCGGG-3' and
            5'-ATTCTAGAGCCGAGCGGCACATG-dT(30)NN-3'. Library was
            constructed using the Clontech Creator SMART kit and
            size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Query Match 16.4%; Score 433.4; DB 6; Length 876;
Best Local Similarity 71.2%; Pred.No. 5.4e-108;
Matches 623; Conservative 0; Mismatches 231; Indels 21; Gaps 3;

QY 1040 GATCCTGTATACATCTGGAGTTCGACATATCAGGCTCTCCCTTACATATGAGACTGGAG 1099
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GTTCTTGTAGGCATCTGGAAATTCGACATATCTGGCACTGGACTTACATATGAACAGGAG 60
QY 1100 ATCATCTTGGTGTATTGTCTGACAACCTGGCATGAAATCTGCGAGGAAGCAGGAACTGT 1159
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 61 ATCATGTTGGTGTGTACTGTGAGAACTCCCTGAAACACAGTGGAGGAGGCTGAAAGTTGT 120
QY 1160 TGGGTCAACCCCTCGGATTTGCTGTTTCAATTACACGGATAAAGAGACGGGTCAACCCC 1219
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 TAGGTTTTTACCAGATGTTTACTTTTCCATTATACCGAAAGAGAGGATGGCACACCAC 180
QY 1220 ---AGGGAAGCTCATTTACCACCTCTTTCCAGGTCCTTGCACCTTTACGATCTGCCCTAG 1276
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 TTAGTGGAAAGCTCTTTGTCACTCTCTTTCCCA---CCATGCACTTTTAAAGACACAGCACTAA 237
QY 1277 CAGCTATCTGATCTTTTGAATCTCTAGAAAAGGCTTCTCTGATTTGCTGTCTCGCTC 1336
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
238 CTCGGTATCGAGATGTTTGTAGTTCTCCCAAAAAGTCTGCTTTGGTGTCTAGCCGCC 297
QY 1337 ATGCATCTGTACCCAGTGAAGCAGAGAGATTGCGCTTTTGTTCATCACCTCTGGGAAAGA 1396
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
298 ATGCTTCTGATCCCACTGAAGCTGATAGTTTGAATAATCTTGCATCTCTCTCTGGAAGG 357
QY 1397 ATGAGTATTCAAATGGGTAGTTGGNAGTCAGAGGATCTTTTGGAGATCATGGCCGAGT 1456
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
358 ATGAATATGCACAATGGGTAGTTGCAAGTCAGAGAAGTCTCTCTTGAGATAATGGCTGAAT 417
QY 1457 TTCCATCAGCAAAACCCCTCTTGGTGTCTTCTTGTCTCAGTAGCCCTCGCTTACCGC 1516
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
418 TCCCATCAGCCAGGCTCCACTTGGAGTTTCTTTCAGCAGTGTGCTCCACGCTTCGAGC 477
QY 1517 CTCGATATCTATTTCTATCTCATCTCTCTTAAAGTTTGTCTCCCTCAAGAAATTCATGTACGT 1576
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
478 CCAGATATTTATTCATATCATCTTCCCAAGATGCTGTCATCTAGAAATTCATGTCACTT 537
QY 1577 GTGCTTTAGTATATGTTCAAAGCCCTACCGAAGGTTTACCAGAGAGTGTGTTCCACAT 1636
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
538 GTGCTTGGTTTGTGATAAGATGCCACAGGACGGAATTCACAAAGGATTTTGTTCAACTT 597
QY 1637 GGATGAAGCATGCAGTCTCTCAGGA-----TAGCTGGGCTCTTATTTTGG 1681
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
598 GGATGAAGTATGCTGTGCCCTTGGAGGAAGCAAGATTCAGCTGGGCGCCAAATTTTGG 657
QY 1682 TTGGAACGTCAAACCTTCAAGTTTACCAGTGCAGCCCTCAACTCCAATTATCATGTTGGGAC 1741
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
658 TTAGGCAATCCAACTTCAAACCTTCTCTGTGATCTTCACTGCGGATTAATCATGATTGGCC 717
QY 1742 CTGGTACAGGTTAGCTCCTTTTCAGAGGATTTTCGAGAAAGATGGCCCTCAAGGAA 1801
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
718 CTGGCACCGGATAGCTCCTTTTAGGGGTTTCTCGAGGAAGATTTGCTCTTAAAGAG 777
QY 1802 ATGGTGCTCAACTTGGCCCGCAGCATGCTCTTTTTCGATGTAGGAATCGTAATATGCACT 1861
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
778 CTGGAGCAGAACTAGGATCATCATATATTTCTTTGGATGCAGGAACCGAANAATGGACT 837
QY 1862 TCATTATGAAGACGAACCTTAAACAACTTCGTGGAA 1896
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
838 ACATTATGAAGATGAGCTGAATGGCTTTGTGGA 872

RESULT 6
COI63167 835 bp mRNA linear EST 18-JUN-2004
LOCUS FLDI_39_H09.g1_A029 Root flooded Pinus taeda cDNA clone
DEFINITION FLDI_39_H09_A029 5', mRNA sequence.
ACCESSION COI63167
VERSION 1
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 835)
AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C. and
Dean,J.F.D.
TITLE An EST database from flooded loblolly pine (Pinus taeda) roots
JOURNAL Unpublished (2004)
COMMENT Contact: Cordonnier-Pratt MM
```


Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (GAGAAACAGCTATGACC).

FEATURES

source

1. .835
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="3 CCLONES"
/db_xref="taxon:3352"
/clone="FLD1_39_H09_A029"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Root flooded"
/notes="Organ: root; Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Prior to harvesting tissues for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain 5% soil moisture content. Pots holding the rooted cuttings were fully submerged in water for 24 hours prior to harvest of the roots for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 16.2%; Score 428.8; DB 7; Length 835;
Best Local Similarity 71.2%; Pred. No. 9.9e-107;
Matches 587; Conservative 0; Mismatches 222; Indels 15; Gaps 1;

QY 1222 GGAAGCTCATTACCACTCTTTCCAGGTCCTTGACACCTTACGATCTCCCTTAGCACGC 1281
DB 12 GGGAGCTCTTGGCACCACCTTCCCTGGTCCATGCACCTGCGAGACTGCTCTTGTCTGT 71

QY 1282 TATGCTGATCTTTTGATCTCTAGAAAGGCTTCTGATGCTCTGCGCTATGCA 1341
DB 72 TTTGCGAGATTGTTGAATCTCTCGAAAGGCTGCTTGGTTGATGCTAGTCAATGCA 131

QY 1342 TCTGTACCCAGTGAAGCAGAGATGTCGCTTTTGTGATCACCCTCTGGAAAGATGAG 1401
DB 132 TCTGATCCAGCTGAAGCTGAGAGTTGAAGTTCTTTTCATCACCAGCCGGAAGATGAG 191

QY 1402 TATTTCAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGCGCCAGTTTCCA 1461
DB 192 TACTCCCAATGGATTACTGTGAGTCAAGAGGCTTTTGAAGTAATGCGAAGATTTCCG 251

QY 1462 TCAGCAAAACCCCTCTTGGTGTGTTCTTGTGAGTACGCGCTCGCTTACGCGCTCGA 1521
DB 252 TCTGCAAAACCCCTCTCGGTGTCTTCTTTGGACAAATTCGCCACGCTCGCAACCTCGA 311

QY 1522 TACTATTCTATCTCATCTCTCTCTAGTTTGTCCCTCAAGAAATTCATGTGAGCTGTGCT 1581
DB 312 TATTACTCTATTTCCTCTCTCTCAAGTTTGGACCAATAGATATCATGTAGCTGTGCT 371

QY 1582 TTAGTATATGGTCAAGCCCTTACCGGAAGGGTTTACCGAGGAGTGTGTTTCGACATGGATG 1641

DB 372 CTGGTTTATGGCGCTAGTCCAACTGGCAGAAATCCACAAAGGTGTTTGTTCCTCAATTCGATG 431
QY 1642 AAGCATGCAAGTTCTCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGA 1686
DB 432 AAGAATTCGGTGGCTCTCTGAGGAAATCCTTGAATGTAGCTGGGCACCACTCTTTGTGTGA 491
QY 1687 AGCTCAAACTTCAAGTTTACCAGCTGACCTCCCTCAACTCCAAATATATCATGTGGGACCTGGT 1746
DB 492 CAGTCANATTTCAATTTGCAGAGATCTTTCAGTTCCTATTTATGTTGGGCGCTTGA 551
QY 1747 ACAGGTTAGCTCTTCTTCAAGAGATTTTCGAGGAAAGAAATGCGCCCTCAAGGAAATGGT 1806
DB 552 ACTGGTTTACGACCTTTTACAGGTTTTCGAGGAAAGAGCCGCACTTCAAGAATCTGGA 611
QY 1807 GCTCAACTTGGCCGACGAGTCTTTTTCGAGTGTAGGAATCGTAATATGGATTCATT 1866
DB 612 GCGAAGCTCGGGCCAGCTGTTCTTTTCTTTGGTGAGGAATCGCCAAATGGACTACATT 671
QY 1867 TATGAAGACGAATAAACAACCTTCGTGGAACGAGGAGTCAATTCGGGAGCTAGTTATTGCC 1926
DB 672 TATGAAGATGAATGAGAACTATGTGGATATCTGGGCTATTCACCGATCTTGTTCCTGCT 731
QY 1927 TTTTCACGTGAAGGGGAAAGAAAGAAATATTTTCAACATAGATGATGAGAAAGCAACG 1986
DB 732 TTTCTCTCGTGAAGGAGCAACCAAGAGATATGTGCAGCACAGATAGCAGAGAGGCATCC 791
QY 1987 GATGTATGCAATGTGATATATCAGGGGACGCTTATCTCTATGTGTG 2030
DB 792 TACATTTGGAATCTCATTTCTCAAGGTGGCTATCTCTATGTATG 835

RESULT 7

CO254258

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .893

/organism="Picea glauca"

/mol_type="mRNA"

/cultivar="PG-29"

/db_xref="taxon:3330"

/clone="WS00821_M14"

/sex="Hermaphrodite"

/tissue type="Early season xylem harvested June 15th, mid season xylem harvested July 10th and late season xylem"

CO254258

WS00821.B21_M14 WS-X-N-A-9 Picea glauca cDNA clone WS00821_M14 3', mRNA sequence.

CO254258

EST.

Picea glauca (white spruce)

Picea glauca

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.

Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R., Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G., Babakiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.

The spruce transcriptome: Analysis of expressed sequence tags from multiple cDNA libraries

Unpublished (2004)

Contact: Joerg Bohlmann

Genome BC forest genomics program

University of British Columbia

UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237, Vancouver, British Columbia, Canada, V6T 1Z3

Tel: 1-604-822-0282

Fax: 1-604-822-6097

Email: bohlmann@interchange.ubc.ca

Plate: WS00821 row: M column: 14

High quality sequence stop: 893.

Location/Qualifiers

1. .893

/organism="Picea glauca"

/mol_type="mRNA"

/cultivar="PG-29"

/db_xref="taxon:3330"

/clone="WS00821_M14"

/sex="Hermaphrodite"

/tissue type="Early season xylem harvested June 15th, mid season xylem harvested July 10th and late season xylem"

harvested August 17th"
/lab_host="E. coli DH10B cells"
/clone_lib="WS-X-N-A-9"
/notes="Organ: Outer xylem from 25 year old trees harvested
at Kalamalka Research Station in Vernon, British Columbia
in 2001; Vector: pBluescript II SK (+) XR; Site 1: EcoRI
(5' end of cDNA); Site 2: XhoI (3' end of cDNA); mRNA was
isolated from each tissue source independently and equal
quantities of mRNA from each tissue were then pooled. cDNA
was prepared from 5 micrograms of mRNA and directionally
ligated into the pBluescript II SK (+) XR vector using the
pBluescript II XR cDNA Library Construction kit according
to manufacturer's instructions with modifications
(Stratagene). Plasmid DNA was then transformed by
electroporation into DH10B cells (Invitrogen) for
propagation. Normalization was applied according to
published methods (Bonaldo M.F. et al. (1996) Genome
Research 6(9):791) in order to reduce the abundance of
highly expressed transcripts."

ORIGIN

Query Match 16.1%; Score 426.4; DB 7; Length 893;
Best Local Similarity 70.0%; Pred. No. 4.7e-106;
Matches 596; Conservative 0; Mismatches 241; Indels 15; Gaps 1;

QY	1353	TGAGCAGAGAGATTGGCTTTTGTTCATCACCCTCTGGGAAGATGAGTATTCAAAATG	1412
DB	3	TGAAGTGGAGAGGTTGAAGTTCTTTCATCACCACCGGAAGGATGAGTACTCCCAATG	62
QY	1413	GGTAGTTGGAAGTCAGAGAGTCTTTGGAGATCATGGCGAGTTCCTCATCAGCAAAAC	1472
DB	63	GATTACTGTGATCAAGAAGTCTTTTAGAAGAAATGGCAGAGTTTCCATCTGCAAAACC	122
QY	1473	CCCTCTGTGTGTTCTTTGCTGCAGTAGCCCTCGCTTACCGCCCTCGATATTTCTAT	1532
DB	123	ACCTATTGGTGTCTCTTTTGCAGCAATTCGCCCGCTCTGCAACCTCGATATTTCTAT	182
QY	1533	CTCATCTCTCTAAGTTTGTCTCCCTCAAGAATCATGTGACGTGCTTTAGTATATGG	1592
DB	183	TTCTCTCTTCCCAAGTTTTCACCCCAATAGATACATGTACATGTGCTCTGGTTATGG	242
QY	1593	TCAAGCCCTACCGAAGGTTTCAACGAGAGTGTCTGCATGATGATCAAGATCAGTCA	1652
DB	243	GCCAGTCCAACTGGCAGATCCATAAAGTGTGTGTTTCAATTGATGAAGATTCAGT	302
QY	1653	TCCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACGTCAAACTT	1697
DB	303	GCCTTCTGAGAAAAGCCATGATTGTAGCTGGGCACCACTTTTGTTCAGACAGTCAA	362
QY	1698	CAAGTTACAGCTGACCCCTCAACTCAATTCATGTGGGACCTGGTACAGGGTTAGC	1757
DB	363	CAAAATGCCAGCAGATCTTCGGTTCCTATTTGTATGTTGGGCCCTCGAACTGGTT	422
QY	1758	TCCTTTTCAGAGATTTCTGCAGAAAGATGGCCCTCAAGGAAATGGTGTCAACTGG	1817
DB	423	ACCTTTTACAGGCTTTTTCGAGAAAGGATGATGATTCAGATCTCGAGAGAGCTTG	482
QY	1818	CCAGCAGTGTCTTTTTCGGATGTAGGAATCGTAATATGGAATTCATTTATGAAGACA	1877
DB	483	GCAGCTGTCTTTTCTTTGGCTGCAGGAATCGCCAAATGGACTACATTTATGAAGATCA	542
QY	1878	ACTAAACACTCTGTGAAGGAGTCAATTCGGAGCTAGTTATTTGCCCTTTTCAGTGA	1937
DB	543	ACTGAAGAACTATGTGGATAATGGTGTATTTAGTGTATCTGGTCTTCTCTCGCA	602
QY	1938	AGGGGAAAAGAGGAATATGTTCAATAAGATGATGGGAAGCAACGATGTATGGAA	1997
DB	603	AGGAACACCAAGAGATGTGCAGACCAAGATTACAGAAAGGCACTCTATTTTGGAA	662
QY	1998	TGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTGTATGCCAAGGGAAATGCCACA	2057
DB	663	TCTTATTTCTCAAGGTGGCTATCTCTATGTGTGTGTGTATGCCAAGGGCAATGGCTAG	722

QY	2058	TGTCATCCGACGTTGCATATCCATTGCCCAAGAACAGGAGCCATCGAATCATCTCTGTC	2117
DB	723	TGTGCACAGGACGCTACACAATATTTGTCCAGAGCAGGAATCAGTGGATAGCAGCATGC	782
QY	2118	CCAAGCTGCAGTAAAGAACTCCAAGTTGCAAGAACGATATCTTAAGAGATGTCTGTGATC	2177
DB	783	AGAGGCTCAGTGAAGAAATTTACAGACAGAGAGATATTTACGAGATGTATGGTAGTT	842
QY	2178	GAATGTAGCTTG 2189	
DB	843	GAGTGAATTTTG 854	

CO166163 806 bp mRNA linear EST 18-JUN-2004
FLD1_59_F08.g1_A029 Root flooded Pinus taeda cDNA clone
FLD1_59_F08_A029 5', mRNA sequence.
CO166163
EST.
SOURCE
ORGANISM
Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Pinaceae; Pinus; Pinus.
REFERENCE
AUTHORS
1 (bases 1 to 806)
Pratt, L., Cordonnier-Pratt, M. M., Lorenz, W. W., Zimmermann, C.,
Johnson, H., Anfuso, C., Kamran, D., Chhabra, D., and Dean, J. F. D.
A loblolly pine (Pinus taeda) EST database from flooded roots
Unpublished (2004)
Other ESTs: FLD1_59_F08.b1_A029
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz (School of
Forest Resources, University of Georgia); plant material prepared
by Craig Zimmermann (School of Forest Resources, University of
Georgia) using rooted cuttings provided by the Forest Biology
Research Cooperative (FBRC) and the CCLONES project at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).
Location/Qualifiers
1..806
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="3 CCLONES"
/db_xref="taxon:3352"
/clone="FLD1_59_F08_A029"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Root flooded"
/note="Organ: root; Vector: pSL1180; Site 1: EcoRI;
Site 2: XhoI; The library was prepared from polyA+ RNA
from the roots of 1-year-old loblolly pine (Pinus taeda)
cuttings that were rooted and then planted in washed sand.
Prior to harvesting tissues for RNA isolation, the rooted
cuttings were maintained for 27 days (April 2003) under
ambient conditions in a local greenhouse. They were kept
on a weekly regimen of 0.5x nutrient-complete Hoagland's
solution and supplemented with additional water sufficient
to maintain 5% soil moisture content. Pots holding the
rooted cuttings were fully submerged in water for 24 hours
prior to harvest of the roots for RNA isolation.
Double-stranded cDNA was cloned unidirectionally into
pSL1180. Inserts can be excised with EcoRI (5' end) and
XhoI (3' end)."

QY 1621 GGAGTGTTCGACATGATGACGATCGAGTTCC-----TCAGGATAGC 1665
Db 541 GGTGTTGTTCAACTTGGATGAAGAATGCTGTCTCGGGGAAAAAGCGATGATCGAGC 600
QY 1666 TGGGCTCCTATTTTGTTCGAACGTCACAACTTCAAGTTACCACTGACCCCTCAACTCCA 1725
Db 601 TGGGACCCATTTTGTTCAGGCAATCAAACTTTAACTTCTTCAAGTGTAAAGTGCC 660
QY 1726 ATTATCATGTGGGACCTGTCAGAGGTAGCTCCTTTTCAGAGGATTTCTGCAAGGAAAGA 1785
Db 661 ATCATATGATGTCGCTGCTGATGCTGCTTTCAGGGGATTCCTTTCAGGAAAGG 720
QY 1786 ATGGCCCTCAGGAAATGCTGCTCAACTTGGCCGACGAGTGTCTTTTTCGATGATAGG 1845
Db 721 CTTGCACTGAAGAAAGCTGCTGCTGAGTTGGGTCCATCTGTATTGTTTTCGCTGCAGA 780
QY 1846 AATCGTAATATGACCTTATTTATGAAGACGAACTAAACAACTTCTGTGGAACGAGGATC 1905
Db 781 AACCGGAAATGATTTTATATATGAGATGAGCTCAACAACTTTGTCAACAGTGTGCA 840
QY 1906 ATTTCGAGCTAGTTATGCTTTTTCAGCTGAAGGGGAAAGAAAGAAATATGTCA 1961
Db 841 CTATCTGAGCTTGTGTTGCTTTTTCAGCTGAGGGACCTACCAGGGAATATGTGCA 896

RESULT 10

CK271587
LOCUS
DEFINITION
EST717665 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAD011 5' end, mRNA sequence.
CK271587
VERSION
KEYWORDS
SOURCE
ORGANISM
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 928)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST717666
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
1..928
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAD011"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="potato abiotic stress cDNA library"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions

and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d, and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

Query Match 15.8%; Score 418.8; DB 7; Length 928;
Best Local Similarity 68.6%; Pred. No. 6e-104;
Matches 608; Conservative 0; Mismatches 272; Indels 6; Gaps 2;
QY 337 GAAGTTGATCTCGGTAAATAAAGCTCACTATATATTTTGGTACTCAGACTGTACTGTCT 396
Db 36 GAGATTGATGATGAAAGAAAGGTTACCATATTTTCGGAACCCGACTGGTACAGCA 95
QY 397 GAAGGATTTGCTAAGGCATTGGCAGAGAAATTTAAGGCAAGATACAAAGAAAGCAGTTGT 456
Db 96 GAAGGCTTCGAAAGGCACTTCTGAGGAAGCAAGGCCAGATATGAGAAGGCTGTCTTT 155
QY 457 AAAGTAGTTGACCTGGATGACTATGCGCGGAGGATGATCAATATGCAAGAGAAATTAAG 516
Db 156 AAAGTCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 215
QY 517 AAAGAGTCTTTGCTGTTTTCATGTTAGTGCCTTATGTTGATGTTGATGATGATGATGAT 576
Db 216 AAAGAGAAATTTGCTGTTTCTTTTCTGGCGCATATGAGAGTGGTGAACCACTGATAT 275
QY 577 GCTGCGAGATTTTCAAAATGTTTCACTCAGGAACATGAAAGGGGAGAGTGGCTTCAGCAA 636
Db 276 GCTGCGAGATTTTCAAAATGTTTCTGAGAGGGGAAAGAGAGGGGTGACTACTTTTAAAT 335
QY 637 CTAACTTATGTTGTTTGGTTGGTAACTGATACGAGCATTTCAACAGATCGCG 696
Db 336 CTTTCAATGATGAGATATTTGGGCTTGGTAAACAGGCAATACGAGCATTTTAAACAGAT 395
QY 697 GTAGATGTTGGATGAGCAACTCGGTAAACAAAGGTGCAAGCGCATTTGTTCAAGTGGGCTC 756
Db 396 AAAGTTGTTGGATGAGCTTCTGCTGAGCAAGGGGCGAGAGGCTTGTTCAGTGGGTCTT 455
QY 757 GTGACGATGATCAATGCAATGAAGATGATTTTATGCTTTGGCGAGAAATGTTGTGGACT 816
Db 456 GGAGATGATGATCAATGCAATGAAGATGATTTTGTGCTGATGCGGTGAGTTACTGTGGCCT 515
QY 817 GAATTGGATCAGTTGCTCAAGATGAGGATGCTGCTCCTTTCAGTGGCTACACCGTATATT 876
Db 516 GAATTGGATAAGTTGCTTCTTGTGGGATGATGCAACT--GCTGCAACTCCATATACT 572
QY 877 GCTACTGTTTCTGAAATACAGGGGTAGTGATTCACGAAACTACGGTCCGGCTCTGGAATGAT 936
Db 573 GCTGCAATTTTGAATATAGGTTATTACCTATGAGAAGTCCCACTTTTGATAACGACTTG 632
QY 937 AAACACATAAA---TACTGCTAACGGGATGTTGCAATTTGATATTTCTCATCTCTTCAGCA 993
Db 633 ACCAACACAAATGGTCACTCAAAATGGACATGTCATTTGTTGATGAACTGGTGCATCATGTT 692
QY 994 ACCATTGTTGCTCAACAAAGAGAGCTCCACAAACCAAGTCTGATAGATCTCTGTATACAT 1053
Db 693 GCTAATGTTGCTGTGAGGAAGAGCTTCATACCGAGCTTCTGATCGTTCTTGTGCACTCAT 752
QY 1054 CTGGAGTTTCGACATATCAGGCTCTTCCCTTTACATATGAGACTGGAGATCATGTTGGTGT 1113
Db 753 CTGGAGTTTGACATTTCTGSCACTGACCTTGTGTATGAACTGGTGCATCATGTTGGTGTG 812
QY 1114 TATGCTGAGAACTCGATGAATACTGTCAGGAGCAAGGGAAGCTGTTGGGTCAACCCCTG 1173
Db 813 TACTGTGAAATTTTATTGAAACCGGTGGAGGAGCTGAAAGGTTACTGAATATATCACCG 872
QY 1174 GATTTGCTGTTTCAATTCCACGGGATAAAGAGCGGGTCAACCC 1219

QY 1518 TCGATACTATTCTATCTCATCTCTCCTAAGTTTGCTCCCTCAAGAATTCATGTGACGTG 1577


```
Db      843 NTCTANGTGAT 853
|||||
3' mRNA sequence.
CO109078.1 GI:48807764
Gossypium raimondii
Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 824)
Kim H., Yu Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and
Wing, R. A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 0041 row: E column: 04.
Location/Qualifiers
1. 824
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Eb0041E04"
/tissue_type="floral"
/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_Eb"
/notes="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."

FEATURES
source
1. 824

ORIGIN
Query Match 15.5%; Score 411; DB 7; Length 824;
Best Local Similarity 70.6%; Pred. No. 8.3e-102; Indels 18; Gaps 2;
Matches 584; Conservative 0; Mismatches 225;

QY 1226 GCTCATTACACCTCTTTCCAGGTCCTTGACCTTAGCATCTGCCCTAGCACGCTATG 1285
Db 1 GTTCTTTGCCCTCTCTCTTTCCCA--CCTCGCTCTTAAGGACAGCACTGGCAGCATG 57

QY 1286 CTGATCTTTGAATCTCTCTAGAAAGCTTCTTGATGCTCTGTCGCTCATGCACTCG 1345
Db 58 CTGATCTTTGAGCTCACCAAAAAGTCTGTTTACTTGTCTGCTGGCTGCTCATGCCCTCG 117

QY 1346 TACCCAGTGAAGCAGAGAGATTGCGCTTTTGTGCATCACCTCTGGGAAAGAATGAGTATT 1405
Db 118 ATCCCACTGAGCTGATCGACTAAGACACCTTCGATCGCCAGCTGGAAAGGATGAATAG 177

QY 1406 CAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG 1465
Db 178 CACAATGGATGGTTGCAAGTCAGAGAAGCCTCTTGAGGTCTATGGCTGAATTTCCCTTCG 237

QY 1466 CAAAACCCCTCTTGGTGTGTTCTTTTGTGTCAGTAGCCCTCGCTTACCGCTCGATCT 1525
Db 238 CCAAGCCTCCACTGGCGTCTTTTGTGAGCCATTCGCCACCGGTTGCAGCCAGATCT 297

QY 1526 ATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAATTTCATGTGAGTGTGCTTTAG 1585
|||||
```

298 ATTCTATCTCATCTCTCAACAAGATGGACCAATCTAGGATTTCATGTAACCTTGTGCATTGG 357

1586 TATATGTCACCAAGCCCTACCGAAGGGTTTCACCGAGGAGTGTGTTTCGACATGATGAAGC 1645

358 TTTTATGAGAAAAACACCAACAGTGTGTTTCAACAAGAGAGTGTGTTTCAACTTGGATGAAGA 417

1646 ATGCAGTTCCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACGT 1690

418 ATTCCACACCATTTGGGACAAATAGCCATGACTGCAGCTGGGCACCTATTTTGTGACGCAAT 477

1691 CAAACTTCAAGTTTACCAGCTGACCCCTCAACTCCCAATTATCATGGTGGGACCTGGTACAG 1750

478 CAAACTTTAAACTTCTTCAAACACTAAAGTGCCTAATTATGATTTGGCCCTGGTACTG 537

1751 GGTAGCTCCTTTCAAGAGGATTTCTGCAGGAAGAATGCCCTCAAGGAAAAATGGTGCTC 1810

538 GATTGGCTCCTTTTCAGGGGATTTCTTCAGGAAGACTTGCCTTAAAGAAGCTGGAGCTG 597

1811 AACTTGGCCCGCAGCAGTGTCTTTTTCGGATGTAGGATCGTAATATGGGACTTCATTTATG 1870

598 ATCTGGGTCCATCTGTATTGTTCTTTTGGCTGCAGGAACCGGAAAAATGGATTACATTTATG 657

1871 AAGACGAACCTAAACAACCTTCGTGGAACGAGGAGTCAATTTTCGGAGCTAGTTATTGCTCTTT 1930

658 AGATGAGCTCAACAACCTTTGTCAACAGTGTGTCACCTTTCTGAGCTTGTGGTGTGCTTTT 717

1931 CACGTGAAGGGGAAAAAGGAATATGTTTCAAATAAGATGATGGAGAAAGCAACGATG 1990

718 CACGCGAGGAGCTTACCAAGGAATATGTGCAACATAAAATGATGGAGAAGGCCCTCGGACA 777

1991 TATGGAAATGATATCAGGGGAGCGGTATCTCTATGCTGTGTGGTGTATG 2037

778 TCTGGAACATGATTTCTTGAAGGAGGTACCTATATGTGTGTGTGTATG 824

Search completed: October 19, 2005, 08:45:50
Job time : 7667 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:24:07 ; Search time 455 Seconds
(without alignments)
9526.367 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	807.6	30.5	1863	3	US-09-627-216A-13
2	807.6	30.5	1863	4	US-09-765-873A-13
3	165.6	6.3	2403	4	US-09-023-655-1226
4	118.4	4.5	260	4	US-09-313-294A-2366
5	111.8	4.2	3037	4	US-09-911-781-10
6	111.8	4.2	3037	4	US-10-400-902-10
7	111.8	4.2	4145	3	US-09-302-620B-82
8	111.8	4.2	4145	4	US-09-912-161-5
9	111.8	4.2	4145	4	US-09-911-781-3
10	111.8	4.2	4145	4	US-10-400-902-3
11	108	4.1	4206	3	US-09-302-620B-81
12	108	4.1	4206	4	US-09-912-161-3
13	108	4.1	4206	4	US-09-911-781-2
14	108	4.1	4206	4	US-10-400-902-2
15	103.8	3.9	212	4	US-09-313-294A-2975
16	102.8	3.9	3155	4	US-09-710-279-3424
17	102.8	3.9	4055	4	US-09-710-279-3357
18	100.2	3.8	1890	3	US-09-134-001C-1557
19	98.6	3.7	1887	4	US-09-710-279-2843
20	96.2	3.6	13508	4	US-08-956-171E-120
21	96.2	3.6	13508	4	US-08-781-986A-120
22	91.6	3.5	3701	1	US-08-553-279-1
23	91.2	3.4	640681	4	US-09-790-988-1
24	87.2	3.3	1928	4	US-09-543-681A-2997
25	86.2	3.3	3150	4	US-10-018-730A-3
26	84.8	3.2	170	4	US-09-313-294A-3539
27	84	3.2	1713	4	US-09-248-796A-4447

28	81	3.1	1842	4	US-09-489-039A-2888	Sequence 2888, Ap
29	73.2	2.8	3242	4	US-09-949-016-4215	Sequence 4215, Ap
30	72.8	2.7	3259	3	US-09-318-448-23	Sequence 23, Appl
31	68.6	2.6	1758	4	US-09-248-796A-3408	Sequence 3408, Ap
32	65.6	2.5	307	3	US-09-172-711-24	Sequence 24, Appl
33	64.2	2.4	5057	3	US-08-365-486A-12	Sequence 12, Appl
34	64.2	2.4	5057	3	US-08-880-342-12	Sequence 12, Appl
35	64.2	2.4	5108	1	US-07-642-003-1	Sequence 1, Appl
36	61	2.3	372	4	US-09-248-796A-4446	Sequence 4446, Ap
37	60.8	2.3	4089	1	US-07-908-245-1	Sequence 1, Appl
38	59.2	2.2	382	3	US-08-976-259-78	Sequence 78, Appl
39	59.2	2.2	382	4	US-09-956-004-78	Sequence 78, Appl
40	59.2	2.2	4097	3	US-09-123-708-5	Sequence 5, Appl
41	59.2	2.2	4097	3	US-09-123-624-5	Sequence 5, Appl
42	56.4	2.1	1141	4	US-09-806-708B-22	Sequence 22, Appl
43	55.4	2.1	4079	4	US-09-016-434-1477	Sequence 1477, Ap
44	55.4	2.1	4353	2	US-08-365-486A-18	Sequence 18, Appl
45	55.4	2.1	4353	3	US-08-880-342-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-627-216A-13

; Sequence 13, Application US/09627216A

; Patent No. 6368837

; GENERAL INFORMATION:

; APPLICANT: Sariaelani, Sima F

; APPLICANT: Tang, Xiao-Song

; APPLICANT: Qi, Wei Wei

; APPLICANT: Vannelli, Todd

; APPLICANT: Gatenby, Anthony

; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid

; FILE REFERENCE: BC1009 US NA

; CURRENT APPLICATION NUMBER: US/09/627,216A

; CURRENT FILING DATE: 2000-07-27

; PRIOR APPLICATION NUMBER: 60/147,719

; PRIOR FILING DATE: 1999-08-06

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 1863

; TYPE: DNA

; ORGANISM: Helianthus tuberosus

US-09-627-216A-13

Query Match	30.5%	Score	807.6;	DB	3;	Length	1863;
Best Local Similarity	67.2%	Pred. No.	6.9e-236;				
Mismatches	1197;	Conservative	0;	Mismatches	559;	Indels	24;
Gaps	3;						
QY	415	TTGGCAGAGAAATTAAGGCAAGTACAGAAAGCAGTTGTTTAAAGTACTTGACCTGGAT	474				
DB	1	TTGTTTGAAGAGCGAAAGCGCATATAAGAAAGCTGTGTTTAAAGTGGTTGATTTGGAT	60				
QY	475	GACTATGACGCGAGGATCATCAATATGAAGAGAAATTAAGAAAGAGTCTTTGGTGT	534				
DB	61	GATTATGCTGTGATGATGAGGATGATGAGAGAAATTCAGAGAGAGACATTTGGCTTC	120				
QY	535	TTGATGGTACCACTTATGATGGTGGAGGCAACTGCAATGCTCGGAGATTTTCAAA	594				
DB	121	TTCTTCTTGCTTACATATGAGATGAGTGGAGCAACTGATAATGCTGCAAGATTTTATAA	180				
QY	595	TGGTTCACATCAGAACATCAAGGGGAGAGTGGCTTCAGCAACTACTTATGGTGT	654				
DB	181	TGTTTCCAGGGGAGATATAAGAGTGTGGCTTGAAGAACTTCACATATGGTGT	240				
QY	655	GGTTTGGGTAAACCGTCAATACGACGATTTCAACAGATCCGGTAGATGTGATGACMA	714				
DB	241	GGTCTTGGCAACAACAGTATGACATTTCAACAGATTTGCATTATGTTGATGAGGT	300				
QY	715	CTCGGTAACAAAGGTCAAGGCGCATTTGTTCAAGTGGGCTCGGTGACGATGATCAATGC	774				

Db 301 CTACAGAGAGGGTGCAGAAAGCGCTTTGTTCCAGTTGGCCCTTGGAGATGACGATCAATCA 360
Qy 775 ATTGAAGATGATTTTACTGCTTGGCGAAGATTGTTGGACTGAAATTTGGATGAGTTGCTC 834
Db 361 ATTGAAGATGATTTTCTGCATGGAAGAAATTAGTGTGGCTGAAATTTGGATCAATTCCT 420
Qy 835 AAGATGAGGATGCTGCTCTTCAGTGGCTACACCGGTATATGCTACTGTTCTCGAATAC 894
Db 421 CTTGATGAAGACGACAAGACT--GCTGCCACTCCTTTACACAGCTGCAATTCGGAATAC 477
Qy 895 AGGTAGTGTATTACGAAACTACGGTCGCGGCTCTGGATGATAAACAACATAAATCTGCT 954
Db 478 CGAGTGTGTTTCATGCAAACTGATACGTTTTCGAGAACTCA-----TAGTCAAACT 531
Qy 955 AACCGGAGTGTGATTTGATATTTCTCCATCTTTCAGAAACCAATGTTGCTCAACAAAGA 1014
Db 532 AATGGTCTATCTGTTACGATGCTCAACATCCATGCGAGATCCAACTGGCTGTTTAAAAA 591
Qy 1015 GAGCTCCAAACCCAGTCTGATAGATCTCTGTATATCATCTGAGTTGCAATATCAGGC 1074
Db 592 GAGCTCCATACCCCTGAAATCCGATCGCTCTGCACTCATCTTGAATTTGACATCTCTCAC 651
Qy 1075 TCTTCCCTTACATATGAGCTGGAGATCATGTTGGTGTGTTATGCTGAGAACTCGGATGAA 1134
Db 652 ACTGGACTATCATACGAACTGGGATCACGTCGGTGTCTACTGTGAAACCTTAATTGAA 711
Qy 1135 ACTGTGAGGAAGCAGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCAATTCAC 1194
Db 712 GTAGTGGAGGAAGCTGAGAACTGATAGGATTAACGACGATACTTATTCTCATTTACAC 771
Qy 1195 ACGGATGAAGAACCGGTCACCCAGGGAAGCTCATTAACCACTCTCTTCCAGTCTCT 1254
Db 772 ATTGATAACGAAGATGAACACCACTCGGTGGACCTACATTTGAGCGCTCTCTTCCCTCC 831
Qy 1255 TGCACTTTAGAAAGCATTTGACCAATTAGCGAGATCTGTGAGTTCTCCAAAGATCA 891
Db 832 TGCTGATGCTCTGTCGCTCATGCTATGTTACCCAGTGAAGCAGAGATTTGCGCTTT 1374
Qy 1315 TCTCTGATGCTCTGTCGCTCATGCTATGTTACCCAGTGAAGCAGAGATTTGCGCTTT 1374
Db 892 ACCTTGTCTCTAGTGGCGCATCTCTGTGATGCCACTGAAGCTGATCGACTACAATTT 951
Qy 1375 TTGTCATCACTCTGGGAAGATGAGTATTAATGGTAGTTGGAAGTCAGAGAT 1434
Db 952 CTTGCACTCTCGTAGGCGAAGGATGAATGCTGAATGGATTTGCAACCAAGAAAGC 1011
Qy 1435 CTTTGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTGCTGTTGTTCTTTGCT 1494
Db 1012 CTTCTTGAGTCTATGNAAGCTTTCCGTGAGCTAAACCTCCGCTCGGGTTTCTTTGCA 1071
Qy 1495 GCAGTAGCCCTCGCTTACCGCTCGATATTTCTATCTCATCTCTCTCTAAGTTTGTCT 1554
Db 1072 GCTATTGCCCCGGGTTTGCAGCTCGATACTACTATTCTTCTCTCCCAAGATGGTA 1131
Qy 1555 CCCTCAAGATTCATGTGAGTGTGCTTTAGTATATGTTCAAGCCCTACCGAAGGTT 1614
Db 1132 CCCAACAGGATTCATGTTACGTGTGATAGTTTATGAGAAGACTCCTGGAGTCTGATC 1191
Qy 1615 CACGAGGAGTGTGTTGCAATGGATGAAGCATGCACTTCCCT-----CAG 1659
Db 1192 CACAAGGAATATGCTCAACTGATGAAGATGCTGTGCTTTGACCGAAATCAAGAT 1251
Qy 1660 GATAGCTGGGCTCCTATTTTTGTGTAAGCTGAAAGCTGAACTTCAAGTTACAGCTGACCCCTCA 1719
Db 1252 TGCAGCTCGGACCCATTTTGTGTAGAACTCACTGAACTTCAGACTTCAGCTGACCCCTAAA 1311
Qy 1720 ACTCCAATATATGTGTGGACCTGTTACAGGTTAGCTCTCTTTCAGAGATTTCTGCAAG 1779
Db 1312 GTCCCGGTTATCATGATTGTCCTCGGATCGGATGCTGCTGCTTTCAGAGTTTCTTCAA 1371
Qy 1780 GAAAGAAATGCCCCCTCAAGGAAATGTTGCTCAACTTTGGCCAGCAGTGTCTTTTTCGGA 1839
Db 1372 GAAAGATTAGCTCTCAAGGAATCTGGAAACCGAACTCGGTCAATCCATTTTGTCTTCGGT 1431

RESULT 2

US-09-765-873A-13
; Sequence 13, Application US/09765873A
; Patent No. 6521748
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
; CURRENT APPLICATION NUMBER: US/09/765,873A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Helianthus tuberosus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1764)
US-09-765-873A-13

Query Match 30.5%; Score 807.6; DB 4; Length 1863;
Best Local Similarity 67.2%; Pred. No. 6.9e-236;
Matches 1197; Conservative 0; Mismatches 559; Indels 24; Gaps 3;

Qy 415 TTGGCAGAAAGAAATTAAGCCAAAGTACAAGAACGATGTTAAAGTAGTTGACCTGGAT 474
Db 1 TTGTTTGAAGAGCCGAAGCGGATATGAAAAGCTGTGTTTAAAAGTGGTTGATTTGGAT 60
Qy 475 GACTATGACGCGAGGATGATCAATATGAAGAGAATTAAGAGAGAGTCTTTGGTGT 534
Db 61 GATTATGCTGCTGATGATGAGGATATGCAAGAGAATTCAGAGAGACATTTGCTTTC 120
Qy 535 TTCTAGGTAGCCACTTATGGTATGGTGGAGCAACTGACAAATGCTGCGAGATTTTACAA 594
Db 121 TTCTTCTTGGCTACATATGAGATGCTGAGCAACTGATAATGCTGCAAGATTTTATAA 180
Qy 595 TGGTTCACAGCAATGAAAGGGGAGAGTGGCTTCAGCAACTAATTATGGTGT 654
Db 181 TGGTTTACCAGGGGAGATGATAAGAGGTTTGGCTTGAAGAACTTCACATATGGTGT 240
Qy 655 GGTTTGGGTAAACCGTCAATACGAGCATTTCAACAAGATCGCGTAGATGTGATGAGCAA 714

Db 241 GGTCTTGGCAACAAACAGTATGACATTTCAACAAGATGCAATTAGTGGTTGTAGGGT 300
Qy 715 CTGGTAAACAAAGGTGCAAGCGCATTTGTTCAAGTGGGGCTCGGTGACGATGATCAATGC 774
Db 301 CTACAGAGAGGGTGCAGAGCGTTTGTTCAGTGGCCCTTGGAGATGACGATCAATCA 360
Qy 775 ATTGAAGATGATTTTACTGCTTGGCGAGAAATTGTTGGACTGAATTTGGATGCTGCTC 834
Db 361 ATTGAAGATGATTTTCTGCATGGAAGAAATTAGTGTGGCTGAATTTGGATCAATTCGTT 420
Qy 835 AAAGATGAGGATGCTGCTCTTCAAGTGGCTACACCGTATATTTGCTACTGTTCTCGAATAC 894
Db 421 CTTGATGAAGACGACAAAGACT--GCTGCCACTCTTTACACAGCTGCCATTTCCGGAATAC 477
Qy 895 AGGTAGTGTGATTCACGAACTTACGGTGGCGCTCTGGATGATAAACACATAAATACTGCT 954
Db 478 CGAGTGTGTTTCTGACAACTGATACGTTTTCGAGATCA-----TAGTCAAACT 531
Qy 955 AACGGGATGTTGCAATTTGATATTTCTCCATCTTTCGAGAACCAATTTGTTGCTCAACAAGA 1014
Db 532 AATGGTCAATCTGTTACAGATGCTCAACATCCATGACAGATCCAAAGTGGCTGTTAAAAA 591
Qy 1015 GAGTCCAAACCAAGTCTGATAGATCTCTGTATATCATCTGAGATTCGATATCAGGC 1074
Db 592 GAGTCCATACCCCTGAATCGATCGCTCTGCACTCATCTTGAATTTGACATCTCTCAC 651
Qy 1075 TCTTCCCTTACATATGAGCTGGAGATCATGTTGGTGTATGCTGAGAACTGGATGAA 1134
Db 652 ACTGGACTATCATACGAACTGGGATCACGTCGGTGTCTACTGTGAAACCTTAATGAA 711
Qy 1135 ACTGTGAGGAAGCAGGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCAATTCAC 1194
Db 712 GTAGTGGAGGAGCTGAGAACTGATAGGATTAACGACAGATCTATTTCTCATACAC 771
Qy 1195 ACGGTAAGAAGAGCGGTCAACCCAGGGAAGCTATTACCACTCTTTCCAGGTCCT 1254
Db 772 ATTGATAACGAAGATGGAACACCACTCGGTGGACCTACATTCAGCAGCTCTTTCCCTCCC 831
Qy 1255 TGACCTTTACGATCTGCCCTAGACGCTATGCTGATCTTTGATCTCTCTAGAAAGCT 1314
Db 832 TGACCTTTAAGAAGCAATTTGACCAATTCAGCAGATCTGTGAGTCTTCCCAAAAGTCA 891
Qy 1315 TCTCTGATGCTCTGCTCGCTCATGCTGTATCCAGTGAAGCAGAGATTCGCGTTT 1374
Db 892 ACCTTGCTGCTAGCTGGCATGCTTCTGATGCCACTGAAGCTGATCGACTACAATTT 951
Qy 1375 TTGTATCACTCTGGGAAAGATGATATTTCAAAATGGGTAGTGGAGTCAAGAGT 1434
Db 952 CTTGCACTCTGTGAGGGAAGGATGAATATGCTGAATGATTTGTGCAAAACCAAGAAGC 1011
Qy 1435 CTTTGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTCTTTGCT 1494
Db 1012 CTTCTTGGTCAATGGAAGCTTTTCGTCAGTAAACCTCCGCTCGGGGTTTCTTTGCA 1071
Qy 1495 GCAGTAGCCCTCGCTTACCGCTCGATATTTCTATCTCATCTCTCTCTAAAGTTGCT 1554
Db 1072 GCTATTGCCCCGGTTTGGAGCTCGATATCTATCTATTCTTCTCCCAAGATGGA 1131
Qy 1555 CCTCAAGAAATCATGTGAGCTGTGCTTTAGTATATAGTCAAAAGCCCTACCGAAGGTT 1614
Db 1132 CCCAACAGGATTCATGTTAGCTGTGATTTAGTTATGAGAAGACTCTCTGGAGGTGCTATC 1191
Qy 1615 CACGAGGAGTGTTCGATCGATGATGAGCATGCTGCTCT-----CAG 1659
Db 1192 CACAAAGGAATATGCTCAACCTGGATGAAGAAATGCTGTGCTTTGACCGGAATAAAGAT 1251
Qy 1660 GATAGCTGGGCTCTATTTTGTTCGAACCTGCAAACTTCAAGTTACAGCTGACCCCTCA 1719
Db 1252 TGCAGCTCGACCCATTTTGTAGAACATCGACTTCAGACTTCAGCTGACCCCTAA 1311
Qy 1720 ACTCCAAATATATGTTGGGACTGCTGATGAGGTTAGCTCTTTACAGAGATTTCTGAG 1779
Db 1312 GTCCCGGTTATCATGATTTGCCCTGGAAACCGGGTGTGCTCCGTTTAGAGGTTTCTTCAA 1371

Qy 1780 GAAAGATGSCCCTCAAGGAATATGCTGCTCACTTTGGCCACAGTGTCTTTTTCGGA 1839
Db 1372 GAAAGATGCTCTCAAGGAATCTGGAACCGAACTCGGTCAATCCATTTTGTCTTCGGT 1431
Qy 1840 TGTAGGAATCGTAATATGGAATCTTATTTATGAAGAAGAACTAAACAACTTCGTGGAACGA 1899
Db 1432 TGCAGAAACCGTAAGTGGATTTCAATATGAGAAATGAACCTGAACAACTTTGTTGAAAT 1491
Qy 1900 GGAGTCAATTCGAGCTAGTTATTCCTTTTACGTTGAAGGGAAGAAAGATATGTT 1959
Db 1492 GCGCGCTTTCCGAGCTTACATGCGTCTCTCGGAAGGCGCATCTAAAGAAATACGTG 1551
Qy 1960 CAACATAAGATGATGAGAAAGCAACCGATGATGAAATGATATCAGGGGACGGTTAT 2019
Db 1552 CAACATAAATGAGCCAAAGGCTTCGGATATATGGAACATGCTTTCTGAGGAGATAC 1611
Qy 2020 CTCATGTTGTGTTGATGCCAAGGAATGGCCAGAGATGTCATCGACGTTGCAATCC 2079
Db 1612 TTATACGTTGTGTTGATGCCAAGGATGGCTTAAAGATGTACACCGAACCTTTCACACC 1671
Qy 2080 ATTGCCCAAGAACAGGACCCATCGAATCATCTGCTGCCGAAGCTGAGTAAAGAACTC 2139
Db 1672 ATTGTCAAGAACAGGGAATTTGGATTCCTCTTAAAGCAGAGCTGTATGTGAAGAACTCA 1731
Qy 2140 CAAAGTTGAAGAACGATATCTAAGAGATGCTGCTGATCGA 2179
Db 1732 CAAATGTCGGAAGATACCTCCGTGATTTGTTGATCTA 1771

RESULT 3

US-09-023-655-1226
; Sequence 1226, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700552557H1
US-09-313-294A-2366

Query Match 4.5%; Score 118.4; DB 4; Length 260;
Best Local Similarity 68.5%; Pred. No. 1.2e-25;
Matches 178; Conservative 0; Mismatches 81; Indels 1; Gaps 1;
QY 1890 CGTGAACGAGGAGTCAATTCGAGCTAGTATTGCTTTCACGTGAAGGGGAAAGAA 1949
DB 1 CCTTGAGAGGGCGCTTCTGAGCTAATTTGTCATTTCTCGGGAAGGGCCAAAGAA 60
QY 1950 GGAATATGTTCAACATAGATGATGAGAAAGCAACGAGATGTATGGAATGTGATATCAGG 2009
DB 61 AGAATATGTCAGCATAGATGTTGGAAGAGCCACAGATATTGGAACATCATCTCAA 120
QY 2010 GGAGGTTATCTCTATGTGTGTGTGATGTCAGAGGGAATGCGCAGAGATGTCATCGCAC 2069
DB 121 TGGTGGTTACTTATATGTTTCCGCTGATGCCAAGGGAATGGCTAGAGATGTACACAAAAT 180
QY 2070 GTTGTCATACCATTCGCCAAGAACAGGACCATGGAATCATCTGCTGCCGAAGCTGCAGT 2129
DB 181 GCT-CATACAAATAGTCAGAGCAGAGGATCTTTGGATACTCCAAACCGAGAGCTATGT 239
QY 2130 AAAGAAACTCCAAAGTTGAAG 2149
DB 240 AAAGAGCTGCAGATGGAAG 259

RESULT 5

US-09-911-781-10
; Sequence 10, Application US/09911781
; Patent No. 6673613
; GENERAL INFORMATION:
; APPLICANT: Craft, David L.
; APPLICANT: Wilson, C. Ron
; APPLICANT: Birch, Dudley
; APPLICANT: Zhang, Yeyan
; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
; FILE REFERENCE: U0012 OS/OAIP (1010-49)
; CURRENT APPLICATION NUMBER: US/09/911,781
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 3037
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-09-911-781-10

Query Match 4.2%; Score 111.8; DB 4; Length 3037;
Best Local Similarity 54.3%; Pred. No. 7.4e-23;
Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;
QY 1681 GTTCGAACGTCACAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGA 1740
DB 2044 GTGAGAAGATCCAACTTAAAGTTGCCAAAGAACTCCACCACCCAGTTATCTTGATTGGT 2103
QY 1741 CTGGTACAGGGTTAGCTCCTTTTCAGAGATTTCTGAGAAAGAAATGGCCCTCAAGGAA 1800
DB 2104 CCAGGTACTGGTGTGCGCCCATTTGAGAGTTTCGTTAGAGAAAGAGTTCAACAAGTCAAG 2163
QY 1801 AATGTTGCTCAACTTGGCCCGCAGAGTGTCTTTTTCGGATGTAGGAATCGTAAATATGAC 1860
DB 2164 AATGTTGCTCAATTTGGCAAGACTTTGTTGTTTATGTTTGGTGGCAAGACTCCACAGGAG 2223
QY 1861 TTCATTTATGAAGCAAGAACTTAAACAACCTTCG---TGGAAACGAGAGTCAATTCGGAGCTA 1917
DB 2224 TTTTGTGTAACAAGAAAGATGGCCGAGTACGCTTCTGTTTATGTTTGGTGGAAACCTTTCAGATG 2283
QY 1918 GTTATTGCTTTTCACGTGAAGGGGAA---AAGAAGGAATATGTTCAACATTAAGATGATG 1974
DB 2284 TTTCAATGCTTCTCTAGACAAGACCCATCCAAGAGGTTTACGTCAGGATTAAGATTTTA 2343
QY 1975 GAGAAGCAACCGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGGT 2034
DB 2344 GAAACAGCAACTTTGTGCACCAATTTGTGACGGAAGGTGCCATTTATCTACGTCGTGGT 2403
QY 2035 GATGCAAGGGGAATGGCCAGAGATGTCCATCCGACGTTGTCATACCATTCGCCCAAGAACAG 2094
DB 2404 GACGCCAGTAGAATGGCCAGAGACGTCACAGACCGATCTCCAAGATTTGTTGCCAAAGC 2463

QY 1975 GAGAAAGCAACGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGGT 2034
DB 2344 GAAACAGCAACTTTGTGCACCAATTTGTTGACCGAAGGTGCCATTTATCTACGTCGTGGT 2403
QY 2035 GATGCAAGGGGAATGGCCAGAGATGTCCATCGCACGTTGTCATACCATTCGCCCAAGAACAG 2094
DB 2404 GACGCCAGTAGAATGGCCAGAGACGTCACAGACCGATCTCCAAGATTTGTTGCCAAAGC 2463
QY 2095 GACCCCATGGAATCATCTGTCGCCGAAGCTGCAGTAAAGAACTCCAAGTTGAAGAACGA 2154
DB 2464 AGAGAAATCAGTGAAGACCAAGGCCGCTGAATTTGGTCAAGTCTCTGGAAGTCCAAAATAGA 2523
QY 2155 TATCTAAGAGATGCTCTGGT 2173
DB 2524 TACCAAGAAGATGTTTGGT 2542

RESULT 6

US-10-400-902-10
; Sequence 10, Application US/10400902
; Patent No. 6790640
; GENERAL INFORMATION:
; APPLICANT: Craft, David L.
; APPLICANT: Wilson, C. Ron
; APPLICANT: Birch, Dudley
; APPLICANT: Zhang, Yeyan
; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
; FILE REFERENCE: U0012 OS/OAIP (1010-49)
; CURRENT APPLICATION NUMBER: US/10/400,902
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US/09/911,781
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 3037
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-10-400-902-10

Query Match 4.2%; Score 111.8; DB 4; Length 3037;
Best Local Similarity 54.3%; Pred. No. 7.4e-23;
Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;
QY 1681 GTTCGAACGTCACAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGA 1740
DB 2044 GTGAGAAGATCCAACTTAAAGTTGCCAAAGAACTCCACCACCCAGTTATCTTGATTGGT 2103
QY 1741 CTGGTACAGGGTTAGCTCCTTTTCAGAGATTTCTGACGAAAGAAATGGCCCTCAAGGAA 1800
DB 2104 CCAGGTACTGGTGTGCGCCCATTTGAGAGTTTCGTTAGAGAAAGAGTTCAACAAGTCAAG 2163
QY 1801 AATGTTGCTCAACTTGGCCCGCAGAGTGTCTTTTTCGGATGTAGGAATCGTAAATATGAC 1860
DB 2164 AATGTTGCTCAATTTGGCAAGACTTTGTTGTTTATGTTTGGTGGCAAGACTCCACAGGAG 2223
QY 1861 TTCATTTATGAAGCAAGAACTTAAACAACCTTCG---TGGAAACGAGAGTCAATTCGGAGCTA 1917
DB 2224 TTTTGTGTAACAAGAAAGATGGCCGAGTACGCTTCTGTTTATGTTTGGTGGAAACCTTTCAGATG 2283
QY 1918 GTTATTGCTTTTCACGTGAAGGGGAA---AAGAAGGAATATGTTCAACATTAAGATGATG 1974
DB 2284 TTTCAATGCTTCTCTAGACAAGACCCATCCAAGAGGTTTACGTCAGGATTAAGATTTTA 2343
QY 1975 GAGAAGCAACCGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGGT 2034
DB 2344 GAAACAGCAACTTTGTGCACCAATTTGTGACGGAAGGTGCCATTTATCTACGTCGTGGT 2403
QY 2035 GATGCAAGGGGAATGGCCAGAGATGTCCATCCGACGTTGTCATACCATTCGCCCAAGAACAG 2094
DB 2404 GACGCCAGTAGAATGGCCAGAGACGTCACAGACCGATCTCCAAGATTTGTTGCCAAAGC 2463


```

; GENERAL INFORMATION:
; APPLICANT: Craft, David L.
; APPLICANT: Wilson, C. Ron
; APPLICANT: Eirich, Dudley
; APPLICANT: Zhang, Yeyan
; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
; FILE REFERENCE: U0012 OS/OAAP (1010-49)
; CURRENT APPLICATION NUMBER: US/09/911,781
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-09-911-781-3

```

Query Match	4.2%;	Score 111.8;	DB 4;	Length 4145;	
Best Local Similarity	54.3%;	Pred. No. 9.2e-23;			
Matches 271;	Conservative	0;	Mismatches 222;	Indels 6;	Gaps 2;
Qy	1681	GTTCGACGTCAAACTTCAAGTTACCACTGACCCCTCAACTCCAATTATCATCTGGTGGGA	1740		
Db	2572	GTGAGAAGATCCAACTTTAAGTTGCCAAAGAACTCCACACCCACAGTTATCTTGTATGGT	2631		
Qy	1741	CCTGGGTACAGGGTTAGTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGGCCCTCAAGGAA	1800		
Db	2632	CCAGGTACTGGTGTGCCCCATTGAGAGGTTTCGTTAGAGAAAGAGTTCAACAAGTCAG	2691		
Qy	1801	AATGGTGCTCAACTTGGCCCCAGCAGTGCTCTTTTTCGGATGTAGGAATCGTAATATGGAC	1860		
Db	2692	AATGGTGCTCAATGTTGGCAAGACTTTGTTGTTTTATGTTTGCAGAACTCCACAGGAGC	2751		
Qy	1861	TTCAATTATGAAGACGAACTAAACAATTGCG---TGGAAACGAGAGTCATTTCCGAGCTA	1917		
Db	2752	TTTTTGTACAAGCAAGAAATGGCCGAGTAGCGTCTCTGTTTGGGTGAAAACTTTTGAGATG	2811		
Qy	1918	GTTATTGCGCTTTTCAGTGAAGGGGAA--AAGAAGGAATATGTTCAACAATAAGATGATG	1974		
Db	2812	TTCAATGCGCTTCTCTAGACAAGACCCATCCAGAAGGTTTACGTCACGAGTAAAGATTTTA	2871		
Qy	1975	GAGAAACAAACGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGGT	2034		
Db	2872	GA AAAACAGCCAACTTTGTGCAGAAATGTTGCACGAGGTGCCATTTACTACGCTCTGTGT	2931		
Qy	2035	GATGCCAAGGGAATGCCACAGATGTCCTATCGCACGTTTGCATACCATTGCCCAAGAACAG	2094		
Db	2932	GACGCCAGTAAATGGCCAGACAGCTCCAGACCAACGATCTTCCAAGATTGTTGCCAAAAGC	2991		
Qy	2095	GGACCATGGAAATCATCTGCTGCGCGAAGCTGCAAGTAAGAAATCCCAAGTTGAAGAACGA	2154		
Db	2992	AGAGAAATCAGTGAAGCAAGGCGCGTGAATTTGGTCAAGTCTCGGAAAGTCCAAAATAGA	3051		
Qy	2155	TATCTAAGAGATGTCTGGT	2173		
Db	3052	TACCAAGAAGATGTTTGGT	3070		

```

RESULT 10
US-10-400-902-3
; Sequence 3, Application US/10400902
; Patent No. 6790640
; GENERAL INFORMATION:
; APPLICANT: Craft, David L.
; APPLICANT: Wilson, C. Ron
; APPLICANT: Erlich, Dudley
; APPLICANT: Zhang, Yeyan
; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
; FILE REFERENCE: U0012 OS/OAAP (1010-49)
; CURRENT APPLICATION NUMBER: US/10/400,902
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US/09/911,781
; PRIOR FILING DATE: 2001-07-24

```

```
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 4145
; TYPE: DNA
; ORGANISM: Candida tropicalis
US-10-400-902-3

Query Match      4.2%; Score 111.8; DB 4; Length 4145;
Best Local Similarity 54.3%; Pred. No. 9.2e-23;
Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;

Qy 1681 GTTCGACAGCTCAAACTTCAAGTTACCAGCTGCACCCTCAACTCCAATTATCATCGGTGGGA 1740
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2572 GTGAGAAGATCCAACTTTAAGTTGCCAAGAACTCACACCCCAGTTATCTTGATTTGGT 2631
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1741 CCTGGTACAGGGTTAGTCCCTTTTCAGAGGATTTCTGCAGAGAAAGAATGGGCCCTCAAGGAA 1800
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2632 CCAGGTACTGGTGTGCCCATTTGAGAGGTTTCGTTAGAGAAAAGAGTTCAAACAAGTCAAG 2691
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1801 AATGGTGCTCAACTTGGCCCCAGCAGTGCTCTTTTTTCGGATGTAGGAATCGTAATATGGAC 1860
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2692 AATGGTGTCAAATGTGTGCAAGACTTTGTGTTTATGTGTTGCGAAAACTCCAACGAGGAC 2751
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1861 TTCATTTATCAAGAACCAACTPAAACAACCTTCG---TGGAAACGAGGAGTCATTTCCGAGCTA 1917
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2752 TTTTGTGTAAGCAAGAAATGGCCCGAGTAGCTTCTGTTTGGGTGAAAACCTTTGAGATG 2811
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1918 GTTATTGCCCTTTTCACGTGAAGGGGAA---AAGAAGGAATATGTTCAACATAAGATGATG 1974
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2812 TTCAATGCCCTTCTTAGACAAGACCCATCCAAGAAGGTTTACGTCCAGGATAAGATTTTA 2871
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 1975 GAGAAACCAACGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGGT 2034
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2872 GAATAACAGCAAATTTGTGACAGAAATGTTTGACCGAAGGTGCCATTATCTACGTCGTGGT 2931
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2035 GATGCCAAGGGAATGGCCAGAGATGTCATCGCACTGTGCAATACCAATGTCGCCAAGAACAG 2094
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2932 GAGCCCAAGTAAATGGCCAGAGACGCTCCAGCACACGATCTCCAAGATTTGTGCGCAAAAGC 2991
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2095 GGACCCATGGAATCATCTGCTGCCGAAGCTGTCAGTAAAGAAACTCCAAGTTGAAGAACGA 2154
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2992 AGAANAATCAGTGAAGAACAGGCCGCTGAATTTGGTCAAGTCTCGGAAGATCCAAAATAGA 3051
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 2155 TATCTAAGAGATGCTGGT 2173
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Qy 3052 TACCAAGAGATGTTTGGT 3070
Db | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
```

```

RESULT 11
US-09-302-620B-81
; Sequence 81, Application US/09302620B
; Patent No. 6331420
; GENERAL INFORMATION:
; APPLICANT: Wilson, C. Ron
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOX
; TITLE OF INVENTION: OXIDOREDUCTASE GENES
; TITLE OF INVENTION: HYDROXYLASE COMPLEX O
; TITLE OF INVENTION: RELATING THERETO
; FILE REFERENCE: 3010-16.seq
; CURRENT APPLICATION NUMBER: US/09/302,620B
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Patent In Ver. 2.1

```

; SEQ ID NO 81		; LENGTH: 4206		; TYPE: DNA		; ORGANISM: Candida tropicalis		US-09-302-620B-81	
Query Match		4.1%; Score 108; DB 3; Length 4206;		Best Local Similarity 53.8%; Pred. No. 1.4e-21;		Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;			
QY	1680	TGTTGCAAGCTCAAACTTCAAGTTACCAGCTGACCCCTCAACTCCAAATTATCATGTGTGG	1739						
Db	2544	TGTGAGAGATCCAACTTTAAAGTTGCCAAAGAACTCCACACCCCAAGTTATCTTGATGG	2603						
QY	1740	ACCTGGTACAGGTTAGCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGA	1799						
Db	2604	TCAGGTAAGATCCAACTTTAAAGTTGCCAAAGAACTCCACACCCCAAGTTATCTTGATGG	2663						
QY	1800	AAATGGTGTCAAGTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGA	1859						
Db	2664	GAATGGTGTCAAGTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGA	2723						
QY	1860	CTTCATTTATGAAGCAACTAAACAACTTCG---TGGACGAGGAGTCAATTCGAGCT	1916						
Db	2724	CTTTTGTGTAAGCAAGCAACTAAACAACTTCG---TGGACGAGGAGTCAATTCGAGCT	2783						
QY	1917	AGTTATGCTCTTTTCAGCTGAAGGGGAA---AAGAGGAAATATGTTCAACATAAGATGAT	1973						
Db	2784	GTTCAATGCTCTTCAGCAAGACCCATCCAAAGAGGTTTACGTCAGGATAAGATTTT	2843						
QY	1974	GGAGAAAGCAACGGATGTAATGGAATGTAATCAGGGGACGGTTATCTCTATGTGTGTGG	2033						
Db	2844	AGAAAACAGCCAACTTGTGCAGAGTTGTTGACTGAAGGTGCCATTATCTACGTCGTGG	2903						
QY	2034	TGATGCCAAGGGAATGCCAGAGATGCCATCGACGTTGCATACCAATGCCCAAGAAC	2093						
Db	2904	TGATGCCAAGGGAATGCCAGAGATGCCATCGACGTTGCATACCAATGCCCAAGAAC	2963						
QY	2094	GGACCCATGGAAATCATCTGCTGCCGAACTGCAGTAAAGAAACTCCAAAGTTGTAAG	2153						
Db	2964	CAGAGAAATAGTGAAGACAAAGGCTGCTGAAATGGTCAAGTCTCGAAGGTCCAAATAG	3023						
QY	2154	ATATCTAAGAGATGCTCGT 2173							
Db	3024	ATACCAAGAAGATGTTTGGT 3043							
RESULT 13									
US-09-911-781-2		; Sequence 2, Application US/09911781		; Patent No. 6673613		; GENERAL INFORMATION:			
		; APPLICANT: Craft, David L.		; APPLICANT: Wilson, C. Ron		; APPLICANT: Eirich, Dudley			
		; APPLICANT: Zhang, Yeyan		; FILE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST		; FILE REFERENCE: U0012 OS/OAAP (1010-49)			
		; CURRENT APPLICATION NUMBER: US/09/911,781		; CURRENT FILING DATE: 2001-07-24		; NUMBER OF SEQ ID NOS: 34			
		; SOFTWARE: Patentin version 3.1		; SEQ ID NO 2		; LENGTH: 4206			
		; TYPE: DNA		; ORGANISM: Candida tropicalis		US-09-911-781-2			
Query Match		4.1%; Score 108; DB 4; Length 4206;		Best Local Similarity 53.8%; Pred. No. 1.4e-21;		Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;			
QY	1680	TGTTGCAAGCTCAAACTTCAAGTTACCAGCTGACCCCTCAACTCCAAATTATCATGTGTGG	1739						
Db	2544	TGTGAGAGATCCAACTTTAAAGTTGCCAAAGAACTCCACACCCCAAGTTATCTTGATGG	2603						
QY	1740	ACCTGGTACAGGTTAGCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGA	1799						
Db	2604	TCAGGTAAGATCCAACTTTAAAGTTGCCAAAGAACTCCACACCCCAAGTTATCTTGATGG	2663						
QY	1800	AAATGGTGTCAAGTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGA	1859						
Db	2664	GAATGGTGTCAAGTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGA	2723						
QY	1860	CTTCATTTATGAAGCAACTAAACAACTTCG---TGGACGAGGAGTCAATTCGAGCT	1916						
Db	2724	CTTTTGTGTAAGCAAGCAACTAAACAACTTCG---TGGACGAGGAGTCAATTCGAGCT	2783						
QY	1917	AGTTATGCTCTTTTCAGCTGAAGGGGAA---AAGAGGAAATATGTTCAACATAAGATGAT	1973						
Db	2784	GTTCAATGCTCTTCAGCAAGACCCATCCAAAGAGGTTTACGTCAGGATAAGATTTT	2843						
QY	1974	GGAGAAAGCAACGGATGTAATGGAATGTAATCAGGGGACGGTTATCTCTATGTGTGTGG	2033						
Db	2844	AGAAAACAGCCAACTTGTGCAGAGTTGTTGACTGAAGGTGCCATTATCTACGTCGTGG	2903						
QY	2034	TGATGCCAAGGGAATGCCAGAGATGCCATCGACGTTGCATACCAATGCCCAAGAAC	2093						
Db	2904	TGATGCCAAGGGAATGCCAGAGATGCCATCGACGTTGCATACCAATGCCCAAGAAC	2963						
QY	2094	GGACCCATGGAAATCATCTGCTGCCGAACTGCAGTAAAGAAACTCCAAAGTTGTAAG	2153						
Db	2964	CAGAGAAATAGTGAAGACAAAGGCTGCTGAAATGGTCAAGTCTCGAAGGTCCAAATAG	3023						
QY	2154	ATATCTAAGAGATGCTCGT 2173							
Db	3024	ATACCAAGAAGATGTTTGGT 3043							
RESULT 12									
US-09-912-161-3		; Sequence 3, Application US/09912161		; Patent No. 6503734		; GENERAL INFORMATION:			
		; APPLICANT: David, Krishna		; APPLICANT: Loper, John C.		; APPLICANT: Loper, John C.			
		; APPLICANT: Loper, John C.		; TITLE OF INVENTION: CYTOCHROME b5 GENE AND PROTEIN OF CANDIDA TROPICALIS AND METHODS		; TITLE OF INVENTION: THEREO			
		; FILE REFERENCE: M6368 (1010-35)		; CURRENT APPLICATION NUMBER: US/09/912,161		; CURRENT FILING DATE: 2001-07-24			
		; NUMBER OF SEQ ID NOS: 45		; SOFTWARE: Patentin version 3.1		; SEQ ID NO 3			
		; LENGTH: 4206		; TYPE: DNA		; ORGANISM: Candida tropicalis		US-09-912-161-3	
Query Match		4.1%; Score 108; DB 4; Length 4206;		Best Local Similarity 53.8%; Pred. No. 1.4e-21;		Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;			
QY	1680	TGTTGCAAGCTCAAACTTCAAGTTACCAGCTGACCCCTCAACTCCAAATTATCATGTGTGG	1739						

THIS PAGE BLANK (USPTO)